

Query Match 49.2%; Score 1362; DB 1; Length 615;
Best Local Similarity 51.0%; Pred. No. 1e-85;
Matches 271; Conservative 71; Mismatches 147; Indels 42; Gaps 6;

QY 2 LDIWVAEAVAPWSKTGGLGDTGGLPIELVKGHRVMTIAPRYDQYADAWDTSVVVDI- 60
DB MNLVFGAEMAPWSKTGGLGDTGGLPMAAANGHRVMVSPRYDQYADAWDTSVVSEIK 141
61 MG---EKVRVPHSITKKGVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRFALFC 117
DB MNLVFGAEMAPWSKTGGLGDTGGLPMAAANGHRVMVSPRYDQYADAWDTSVSEIK 136
QY 61 ---MGEKVRVPHSITKKGVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRFALFC 117
DB MNLVFGAEMAPWSKTGGLGDTGGLPMAAANGHRVMVSPRYDQYADAWDTSVSEIK 136
QY 137 VDRYERVRYFHCYKRGVDFVDPHPCFLEKVRGKTEKIYGPAGDTYDQNRFSLLC 196
DB VDRYERVRYFHCYKRGVDFVDPHPCFLEKVRGKTEKIYGPAGDTYDQNRFSLLC 196
QY 118 KAALAEARVLPF-----GP-----GEDCVFVANDHSAVLPVLLKDEYQPK 158
DB KAALAEARVLPF-----GP-----GEDCVFVANDHSAVLPVLLKDEYQPK 158
QY 197 QAALAEVPRILDLNNPHSGPYAMLCRAVPFRAGEDVVFVNCNDWHTGLLACYLKSQSN 256
DB QAALAEVPRILDLNNPHSGPYAMLCRAVPFRAGEDVVFVNCNDWHTGLLACYLKSQSN 256
QY 159 GQFTKAKSVLAHNIAPQGRMEBAFKDTKLPOAFAFKLAFSDCYAKVYVTEATPMEDEK 218
DB GQFTKAKSVLAHNIAPQGRMEBAFKDTKLPOAFAFKLAFSDCYAKVYVTEATPMEDEK 218
QY 257 GIYRTAKVAFCIHNSIYQGRFSDDFDFAQLNLPDRFKSDFIDGYDK----- 303
DB GIYRTAKVAFCIHNSIYQGRFSDDFDFAQLNLPDRFKSDFIDGYDK----- 303
QY 219 PPLTGKYYKKINWLGGLIAADKLVTSVPYATIAADAGGVVELDTVIRAKGIEGVNG 278
DB PPLTGKYYKKINWLGGLIAADKLVTSVPYATIAADAGGVVELDTVIRAKGIEGVNG 278
QY 304 -PVEG---RKINWKGAILQADKLVTSVPYATIAADAGGVVELDTVIRAKGIEGVNG 359
DB -PVEG---RKINWKGAILQADKLVTSVPYATIAADAGGVVELDTVIRAKGIEGVNG 359
QY 279 MDIEWNPKTDFLSAPYDQNSVYAGRAAKAEALQAEGLPVDPTAPLFAFIRGLEQKG 338
DB MDIEWNPKTDFLSAPYDQNSVYAGRAAKAEALQAEGLPVDPTAPLFAFIRGLEQKG 338
QY 360 MDVSEWDPIDKFLTVNDVDTALEGKALNKEALQAEGLPVDPRKVPVLAFIGRLEQKG 419
DB MDVSEWDPIDKFLTVNDVDTALEGKALNKEALQAEGLPVDPRKVPVLAFIGRLEQKG 419
QY 339 VDIILALPKLILATPKVOJAILGNGKAAEKLVAIGTKYGRAGKGVVKSAPLAHMLTA 398
DB VDIILALPKLILATPKVOJAILGNGKAAEKLVAIGTKYGRAGKGVVKSAPLAHMLTA 398
QY 420 PDVMIATPEIVKEEDQVILLGTGKKFERLLKSVEKFPTKRVAVVRFNAPLAHOMMA 479
DB PDVMIATPEIVKEEDQVILLGTGKKFERLLKSVEKFPTKRVAVVRFNAPLAHOMMA 479
QY 399 GADFMLVPSPEPCGLIOLHAMHYGTVPVASTGSLVDTVKGVTFGRHMGALNPD--KLD 456
DB GADFMLVPSPEPCGLIOLHAMHYGTVPVASTGSLVDTVKGVTFGRHMGALNPD--KLD 456
QY 480 GADVLAVTSREPCGLIOLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDNCVVE 539
DB GADVLAVTSREPCGLIOLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDNCVVE 539
QY 457 EADALAAATVRRASEFAGRYPEMVANCSIDLSWSKPAQKWEGLEEV 507
DB EADALAAATVRRASEFAGRYPEMVANCSIDLSWSKPAQKWEGLEEV 507
QY 540 PADVKVVTTLKRAVKVGTGTPAYHEMVKNQMIQDLSWKGPAKNWEDVILEL 590
DB PADVKVVTTLKRAVKVGTGTPAYHEMVKNQMIQDLSWKGPAKNWEDVILEL 590

RESULT 10
TI4731
glycogen(starch) synthase (EC 2.4.1.11) precursor, granule-bound - sorghum
N:Alternate names: starch synthase, granule-bound
C:Species: Sorghum bicolor (sorghum)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2002
C:Accession: TI4731
submitted to the EMBL Data Library, April 1995
R:Hsing, Y.C.
A:Reference number: Z18173
A:Accession: TI4731
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-608 <HS>
A:Cross-references: EMBL:U23945; NID:gl255713; PID:gl255714
A:Experimental source: strain 12311; young seed
C:Genetics:
A:Genome: nuclear
A:Note: Wx
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose producing
A:Pathway: starch biosynthesis
C:Superfamily: starch synthase
C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
F:1-77/Domain: transit peptide (amyloplast) #status predicted <TNP>
F:78-608/Product: UDPglucose-starch glycosyltransferase #status predicted <MAT>

Query Match 49.0%; Score 1355.5; DB 2; Length 608;
Best Local Similarity 50.6%; Pred. No. 2.9e-85;
Matches 276; Conservative 76; Mismatches 154; Indels 39; Gaps 11;

QY 2 LDIWVAEAVAPWSKTGGLGDTGGLPIELVKGHRVMTIAPRYDQYADAWDTSVVVDI- 60
DB MNLVFGAEMAPWSKTGGLGDTGGLPMAAANGHRVMVSPRYDQYADAWDTSVVSEIK 141
QY 61 MG---EKVRVPHSITKKGVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRFALFC 117
DB MGDGYETVRPHCYKRGVDFVDPHPCFLEKVRGKTEKIYGPAGDTYDQNRFSLLC 201
QY 118 KAALAEARVLPF-----GP-----GEDCVFVANDHSAVLPVLLKDEYQPKGFTAKSVLA 169
DB QAALAEARVLPF-----GP-----GEDCVFVANDHSAVLPVLLKDEYQPKGFTAKSVLA 169
QY 202 QAALAEARVLPF-----GP-----GEDCVFVANDHSAVLPVLLKDEYQPKGFTAKSVLA 261
DB QAALAEARVLPF-----GP-----GEDCVFVANDHSAVLPVLLKDEYQPKGFTAKSVLA 261
QY 170 IHNTAFQGRMEEAFKOTKLPOAFAFKLAFSDCYAKVYVTEATPMEDEKPLTKYTKKI 229
DB IHNTAFQGRMEEAFKOTKLPOAFAFKLAFSDCYAKVYVTEATPMEDEKPLTKYTKKI 229
QY 262 IHNTAFQGRMEEAFKOTKLPOAFAFKLAFSDCYAKVYVTEATPMEDEKPLTKYTKKI 304
DB IHNTAFQGRMEEAFKOTKLPOAFAFKLAFSDCYAKVYVTEATPMEDEKPLTKYTKKI 304
QY 230 NMLKGGITIAADKLVTSVPYATIAADAGGVVELDTVIRAKGIEGVNGMDIEWNPKT 289
DB NMLKGGITIAADKLVTSVPYATIAADAGGVVELDTVIRAKGIEGVNGMDIEWNPKT 289
QY 305 NMLKGGITIAADKLVTSVPYATIAADAGGVVELDTVIRAKGIEGVNGMDIEWNPKT 364
DB NMLKGGITIAADKLVTSVPYATIAADAGGVVELDTVIRAKGIEGVNGMDIEWNPKT 364
QY 290 KFLSAPYDQNSVYAGRAAKAEALQAEGLPVDPTAPLFAFIRGLEQKGVDIILALPKI 349
DB KFLSAPYDQNSVYAGRAAKAEALQAEGLPVDPTAPLFAFIRGLEQKGVDIILALPKI 349
QY 365 KYIAVKYDVSTAVEAKALNKEALQAEGLPVDPRKIPVLAFIGRLEQKGPDVMAAIP-L 423
DB KYIAVKYDVSTAVEAKALNKEALQAEGLPVDPRKIPVLAFIGRLEQKGPDVMAAIP-L 423
QY 350 LATPKVQITAILGTGKAAEKLVAIGTKYGRAGKGVVKSAPLAHMLTAGADFMVPSRF 409
DB LATPKVQITAILGTGKAAEKLVAIGTKYGRAGKGVVKSAPLAHMLTAGADFMVPSRF 409
QY 424 LMEEDIQVILLGTGKKFERLLKSVEKFPTKRVAVVRFNAPLAHOMMA 483
DB LMEEDIQVILLGTGKKFERLLKSVEKFPTKRVAVVRFNAPLAHOMMA 483
QY 410 EPCGLIOLHAMHYGTVPVASTGSLVDTVKGVTFGRHMGALNPD--KLD 467
DB EPCGLIOLHAMHYGTVPVASTGSLVDTVKGVTFGRHMGALNPD--KLD 467
QY 484 EPCGLIOLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDNCVVEPADVKVATL 543
DB EPCGLIOLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDNCVVEPADVKVATL 543
QY 468 FRASEFAGRYPEMVANCSIDLSWSKPAQKWEGLEEV--VYKGG-----VATAKE 520
DB FRASEFAGRYPEMVANCSIDLSWSKPAQKWEGLEEV--VYKGG-----VATAKE 520
QY 544 KRAIKVGTGTPAYHEMVKNQMIQDLSWKGPAKNWEDVILEL 603
DB KRAIKVGTGTPAYHEMVKNQMIQDLSWKGPAKNWEDVILEL 603
QY 521 EIKVP 525
DB EIKVP 525
QY 604 NVAAP 608
DB NVAAP 608

RESULT 11

S07314

glycogen(starch) synthase (EC 2.4.1.11) precursor - maize
N:Alternate names: starch synthase; UDP-glucose starch glycosyltransferase, starch gr
C:Species: Zea mays (maize)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 02-Aug-2002
C:Accession: S07314
R:Kloesgen, R.B.; Gierl, A.; Schwarz-Sommer, Z.; Saedler, H.
Mol. Gen. Genet. 203, 237-244, 1986
A:Title: Molecular analysis of the waxy locus of Zea mays.
A:Reference number: S07314
A:Accession: S07314
A:Molecule type: DNA
A:Residues: 1-605 <KLO>
A:Cross-references: EMBL:X03935; NID:g22509; PIDN:CAA27574.1; PID:g1644339
A:Experimental source: line C
A:Note: translation of the nucleotide sequence is not complete
A:Note: part of this sequence, including the amino end of the mature protein, was con
C:Genetics:
A:Gene: waxy
A:Introns: 107/3; 134/3; 167/3; 197/3; 219/1; 252/3; 289/2; 370/3; 431/3; 495/3; 524/3
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose produc
C:Superfamily: starch synthase
C:Keywords: amyloplast; chloroplast; glycogen/starch biosynthesis; glycosyltransferas
F:1-72/Domain: transit peptide (amyloplast) #status predicted <TNP>
F:73-605/Product: glycogen (starch) synthase #status experimental <MAT>

Query Match 48.9%; Score 1353.5; DB 1; Length 605;
Best Local Similarity 50.4%; Pred. No. 3.9e-85;
Matches 275; Conservative 79; Mismatches 153; Indels 39; Gaps 11;


```
Db 248 TLLCYAACAPLILEGGIYQKMEFVNDWHSALVPVLLAAKYRPGVYRDARSVLVI 307
QY 171 HNTAFOGRMEEAFAKDKLFOAARDKLFADSGYAKVYTEATPMEDEKPPLTGTYKKIN 230
Db 308 HNLAAHQGEPASTYDPIGLPPEWYGALEW-----VPEWARRHALDKG-----EAVN 354
QY 231 WLKGGIITAADKLVTSPNYATEIAADAAGGVDELDTVI--RAKGIEGVINGMDIEEWNPKT 288
Db 355 FLKGAIVTADRVTVSGYSMEVIT-ABGGGCLNELLSSRSKSVLNGVINGDINDWNPST 413
QY 289 DKFLSAPYDQNSVYAGKAAAEALQAEGLPVPDTPAPLEAFIFGRLEPKGVDIILAALPK 348
Db 414 DKFLPYHVSVDL-SGRAKCAELQKELGPIRPDPVPLIGTIFGRLDYQKGDILKLAIPD 472
QY 349 ILATPKVQIALLGTGKAAEKLVAIGTKYKGRAGKGVVVKFSAPLAHMLTAGADFMVPSR 408
Db 473 LM-RDNIQFVLMGSDGPFEGWMSSTESGYRDKFRGWGFSVPVSHRITAGCILLMPSR 531
QY 409 FEPGGLIQLHAMHYGTVPVVAASGTGLVDTVK-----EGVTGFHMGALNPDK 454
Db 532 FEPGGLNQLYAMQYGTVPVVGHTGGLRDTVENFNFPAEKGGQIGWAFSPLTIEK 586

RESULT 14
T01208
starch synthase (EC 2.4.1.21) isoform STSII-1 - maize (fragment)
N:Alternate names: starch synthase isoform STSII-1
C:Species: Zea mays (maize)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Aug-2002
C:Accession: T01208
R:Knight, M.E.; Harn, C.; Lilley, C.E.R.; Guan, H.P.; Singletary, G.W.; Mu-Forester, C.;
Plant J. 14, 613-622, 1998
A:Title: Molecular cloning of starch synthase I from maize (W64A) endosperm and expressi
A:Reference number: Z14279; MUID:98340555; PMID:9675904
A:Accession: T01208
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-732 <KNI>
A:Cross-references: EMBL:AF019296; NID:g2811133; PIDN:AAD13341.1; PID:g2655029
A:Experimental source: strain W64A; endosperm
C:Genetics:
A:Gene: SSIIa
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPGlucose producing a
C:Superfamily: starch synthase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 31.5%; Score 872; DB 2; Length 732;
Best Local Similarity 39.7%; Pred. No. 5.8e-52;
Matches 211; Conservative 77; Mismatches 178; Indels 66; Gaps 15;

QY 2 LDIVMVAEVAWPWSKTGGGLGVDYTGGLPIELVKRGRHVMTIAPRYDQYADAWDTSV--VVD 59
Db 241 MNVIVAAECSPWCKTGGGLGVDVGGALPKALARRGRHVMVVPYGYVEAFDGMGRKYYK 300
QY 60 IMGE--KVRYFHSIKKGVHRVWIDHFWFLAK---VWGTGSKLYGPRSGADYLDNHRKFA 114
Db 301 AAGQDLEVNYPHAFIDGVDFVFDAPLFRHRODDIYGGSRQETM-----KRM 348
QY 115 LECKAAIEARVLP-----FGGEDCVFVANDWHSALYVLLKDEYQPKGQFTKAKSVLA 169
Db 349 LECKVAVEVPWHPVPCGGVGYGCG- NLVFIANDWHTALLPVLKAYYRDRHGLMQYTRSLV 407
QY 170 IHNIAFOGRMWEAFKDKTLPOAFAFDKLFASGYAKVYTEATPMEDEKPPLTGTYKKI 229
Db 408 IHNIAHQGRGPVDEFPYMDLPHYLQHFELYD-----PVGG---EHA 446
QY 230 NMLKGGIITAADKLVTSPNYATEIAADAAGGVDELDTVIIRAKG--IEGVINGMDIEEWNPK 287
Db 447 NIFAAGLKMADRVTVTSRGYVWELKT-VGGWGLHDHDIIRSDNWKINGVINGIDHGEWNEK 505
QY 288 TDKFLSAP-----YDQNSVYAGKAAAEALQAEGLPVPDTPAPLEAFIFGRLEPKGVDIIL 343
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Db 506 VDVHLRSQGYTNYSLDTLDAGKROCKAALRELGLGVDRDDVPLIGFIRGLDGQKGVDIIG 565
QY 344 AALPKILATPKVQIALLGTGKAAEKLVAIGTKYKGRAGKGVVVKFSAPLAHMLTAGADEM 403
Db 566 DAMFWI-AGQDVQLVMLGTGRADLERMLQHLEREPNKRGVNGVGEVPMHAHRTAGADVL 624
QY 404 LVPSREFPCGLIQLHAMHYGTVPVVAASGTGLVDTVKE-----GVTFHMGALNPDKLDEAD 459
Db 625 VMPSEFPCGLNQLYAMAYGTVPVVAHVAGGLRDTVAPEDPFGDAGLW-----TFDRAE 678
QY 460 ADALAAIVRRASEVFA--GGRYPEMVAVNCISDLSWSKPAQKWEGLLEEVVY 509
Db 679 ANKLTIALRHCLDTYKRYGESWKSQARGMSQDLSWDHAAELYEDVLVAKY 730

RESULT 15
S01505
glycogen(starch) synthase (EC 2.4.1.11) isoform II precursor - garden pea
N:Alternate names: glycogen(starch) synthase (EC 2.4.1.11) isoform II precursor; gran
C:Species: Pisum sativum (garden pea)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Aug-2002
C:Accession: S61505; S72373; S72312
R:Dry, I.; Smith, A.; Edwards, A.; Bhattacharya, M.; Dunn, P.; Martin, C.
Plant J. 2, 193-202, 1992
A:Title: Characterization of cDNAs encoding two isoforms of granule-bound starch synt
A:Reference number: S61504; MUID:93251108; PMID:1302049
A:Accession: S61505
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-752 <DRY>
A:Cross-references: EMBL:X88790
A:Accession: S72373
A:Molecule type: protein
A:Residues: 58-59, 'H', 61-73 <DRW>
R:Edwards, E.A.
submitted to the EMBL Data Library, June 1995
A:Reference number: S72312
A:Accession: S72312
A:Molecule type: mRNA
A:Residues: 1-85, 'KVLALQRELIIQOIAERKK', 104-139, 'SSSSSAVETKRWHCQQLC', 160-752 <EDW>
A:Cross-references: EMBL:X88790; NID:g887572; PID:g887573
C:Keywords: glycosyltransferase; hexosyltransferase
F:1-57/Domain: signal sequence #status predicted <SIG>
F:58-752/Product: glycogen (starch) synthase .isoform II #status experimental <MAT>

Query Match 31.5%; Score 871; DB 2; Length 752;
Best Local Similarity 38.2%; Pred. No. 7e-52;
Matches 209; Conservative 82; Mismatches 160; Indels 96; Gaps 16;

QY 2 LDIVMVAEVAWPWSKTGGGLGVDYTGGLPIELVKRGRHVMTIAPRYDQYADAWDTSV--VVD 59
Db 261 MNILYSABCAPWSKTGGGLGVDVAGSLPKALARRGRHVMIVAPHYGYAEADHIGVRRKYK 320
QY 60 IMGE--KVRYFHSIKKGVHRVWIDHFWFLAKVWGTGSKLYGPRSGADYLDNHRKFA 117
Db 321 VAGQDMEVYFHYIDGVDFIDISP-----IFENLESNIY-----GSNRLDILRRMVLFC 371
QY 118 KAAIEARVLP-----FGGEDCVFVANDWHSALYVLLKDEYQPKGQFTKAKSVLAH 172
Db 372 KAAVEVPWHPVPCGGICYGCG- NLVFIANDWHTALLPVLKAYYRDRHGLMNYTRSLV 430
QY 173 IAFQGRMWEAFKDKTLPOAFAFDKLFASGYAKVYTEATPMEDEKPPLTGTYKKI 232
Db 431 IAHQGRG-----PVEDFNVDLSGNYLDFKMYDPVGGEH-----FNIF 469
QY 233 KGGIITAADKLVTSPNYATEIAADAAGGVDELDTVIIRAKG--IEGVINGMDIEEWNPKTK 290
Db 470 AAGLKTAADRLVTVSHGYAWELKT-SEGWGLHNLINESDMKFRGIVNGVDTKDNVQFDA 528
QY 291 FLSP-----YDQNSVYAGKAAAEALQAEGLPVPDTPAPLEAFIFGRLEPKGVDIILAAL 346
Db 529 YLTSQGYTNYNLKTLQTKGRQCKAALQRELGLPVPREDVPIISTIFGRLDHKGVDLIAEAI 588
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QY 347 PKILATPKVQIAILLGTGKAAYEKLVAICTYKGRAGVVKFSAPLAHMLTAGADFMVLP 406
Db 589 PWMM-SHDVQLVMLGTGRADLEQMLKEFEAOHCDCKIRSWGVGFSVKMAHRTAGSDILLMP 647
QY 407 SRFEPGLIQLHAMHYGTVPVASTGGLVDIVK-----EGYTGPHMGALNPKLDEADA 460
Db 648 SRFEPGLNQLYAMSYGTVPVHVGVGGLRDTVPFPNPFDESGVGW-----TFDRAEA 699
QY 461 DALAATVRRASEVEFAGGRYPPEWVNCI-----LWNCLLTYDKKSWEGIOERGMSQLDSWDNAAQQYEE 743
Db 700 NKIMAA-----LWNCLLTYDKKSWEGIOERGMSQLDSWDNAAQQYEE 743
QY 503 LLEEVVY 509
Db 744 VLVRAKY 750

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Search completed: June 4, 2003, 14:57:40
Job time : 17.7251 secs

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OM protein - protein search, using sw model

Run on: June 4, 2003, 13:50:41 ; Search time 7.12991 Seconds
(without alignments)
3088.950 Million cell updates/sec

Title: US-09-980-771A-9
Perfect score: 2769
Sequence: 1 ALDIVMAAEVAPWSKTGGL.....GGVATAKKEIKVPAEKIP 531

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1481.5	53.5	608	1	UGST_MANES
2	1457.5	52.6	607	1	UGST_SOLTU
3	1455.5	52.6	608	1	UGST_ANTMA
4	1415.5	51.1	603	1	UGST_PEA
5	1412.5	51.0	608	1	UGST_IPOBA
6	1397.5	50.5	609	1	UGST_ORYSA
7	1395.5	50.4	603	1	UGST_HORVU
8	1394.5	50.4	609	1	UGST_ORYGL
9	1362	49.2	615	1	UGST_WHEAT
10	1355.5	49.0	608	1	UGST_SORBI
11	1353.5	48.9	605	1	UGST_MALZE
12	902.5	32.6	641	1	UGS2_SOLTU
13	873.5	31.5	626	1	UGS2_ORYSA
14	871	31.5	752	1	UGS3_PEA
15	866	31.3	610	1	UGS2_WHEAT
16	847.5	30.6	788	1	UGS3_SOLTU
17	684.5	24.7	477	1	GLGA_STREN
18	677.5	24.5	484	1	GLGA_BACSU
19	670.5	24.2	485	1	GLGA_BACST
20	669	24.2	478	1	GLGA_LACIA
21	653.5	23.6	480	1	GLG1_RHIME
22	652	23.5	480	1	GLGA_AGRU5
23	646.5	23.5	486	1	GLGA_THEME
24	637	23.3	480	1	GLGA_RHTR
25	637	23.0	477	1	GLGA_CLOAB
26	622	22.5	482	1	GLGA_CLOPE
27	622	22.5	484	1	GLGA_VIBCH
28	614.5	22.2	476	1	GLGA_BACHD
29	604.5	21.8	486	1	GLG2_RHIME
30	604	21.8	476	1	GLGA_YERPE
31	602.5	21.8	481	1	GLGA_RHILLO
32	587	21.2	477	1	GLGA_FCOLI
33	587	21.2	477	1	GLGA_SALTI

34	580	20.9	477	1	GLGA_SALTY
35	578	20.9	480	1	GLGA_PASMU
36	569	20.5	476	1	GLGA_HAEIN
37	568.5	20.5	1230	1	UGSA_SOLTU
38	560.5	20.2	472	1	GLGA_ANASP
39	555	20.0	461	1	GLGA_FUSNN
40	552.5	20.0	463	1	GLGA_AQUAE
41	538	19.4	465	1	GLGA_SYN7
42	536	19.4	477	1	GLGA_RHOSH
43	536	19.4	492	1	GLG2_ANASP
44	535	19.3	477	1	GLGA_SINY3
45	527	19.0	444	1	GLGA_DEIRA

ALIGNMENTS

RESULT 1
UGST_MANES

ID UGST_MANES STANDARD; PRT; 608 AA.

AC Q43784;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Granule-bound glycogen [starch] synthase, chloroplast precursor

DE (EC 2.4.1.11).

GN WAXY OR GBSS.

OS Manihot esculenta (Cassava) (Manioc).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Malpighiales; Euphorbiaceae; Manihot.

OX NCBI_TaxID=3983;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. M.COL.22; TISSUE=Tuberous root;

RX MEDLINE=94083565; PubMed=8260633;

RA Salehuzzaman S.N.; Jacobsen E.; Visser R.G.F.;

RT "Isolation and characterization of a cDNA encoding granule-bound

starch synthase in cassava (Manihot esculenta Crantz) and its

antisense expression in potato.";

RL Plant Mol. Biol. 23:947-962(1993).

CC -! FUNCTION: RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE IN RESERVE

CC STARCH.

CC -! CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) -

CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).

CC -! PATHWAY: Starch biosynthesis.

CC -! SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.

CC -! TISSUE SPECIFICITY: SYNTHESIZED IN A NUMBER OF DIFFERENT ORGANS,

CC BUT MOST ABUNDANTLY IN TUBERS.

CC -! SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE

CC FAMILY.

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EMBL; X74160; CAA52273.1; -
InterPro; IPR001296; Glycos_transf_1.
Pfam; PF00534; Glycos_transf_1; 1.
KW Glycogen biosynthesis; Transferease; Glycosyltransferase;
FT TRANSIT peptide; Chloroplast; Starch biosynthesis.
FT CHAIN 79 608 CHLOROPLAST (BY SIMILARITY).
FT BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 608 AA; 66968 MW; C9C970CD3011BDD8 CRC64;

Query Match 53.5%; Score 1481.5; DB 1; Length 608;
Best Local Similarity 55.0%; Pred. No. 2e-92;
Matches 299; Conservative 64; Mismatches 148; Indels 33; Gaps 9;

RESULT 6

UGST_ORYSA STANDARD; PRT; 609 AA.

AC P19395; 043013; (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Granule-bound glycogen [starch] synthase, chloroplast precursor (EC 2.4.1.11).

GN WAXY OR WX.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Seed;

RX MEDLINE=92322986; PubMed=1377969;

RA Okagaki R.J.;

RT "Nucleotide sequence of a long cDNA from the rice waxy gene.";

RL Plant Mol. Biol. 19:513-516(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Japonica Taichung 65; TISSUE=Seedling;

RA Hirano H.Y., Sano Y.;

RT "Molecular characterization of the waxy locus of rice (Oryza sativa).";

RL Plant Cell Physiol. 32:989-997(1991).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Japonica, and cv. Hanfeng;

RX MEDLINE=91016948; PubMed=2216792;

RA Wang Z.Y., Wu Z.L., Xing Y.Y., Zheng F.G., Guo X.L., Zhang W.G., Hong M.M.;

RT "Nucleotide sequence of rice waxy gene.";

RL Nucleic Acids Res. 18:5898-5898(1990).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Indica;

RA Wang X.Q., Wang Z.Y., Hong M.M.;

RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE OF 153-343 FROM N.A.

RX MEDLINE=91200672; PubMed=2016064;

RA Shimada H., Tada Y.;

RT "Rapid isolation of a rice waxy sequence: a simple PCR method for the analysis of recombinant plasmids from intact Escherichia coli cells.";

RL Gene 98:243-248(1991).

CC -!- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.

CC -!- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) = UDP + ((1,4)-alpha-D-glucosyl)(N+1).

CC -!- PATHWAY: Starch biosynthesis.

CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.

CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE FAMILY.

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EMBL; X62134; CAA44065.1; -

DR EMBL; X58228; CAA41186.1; -

DR EMBL; X53694; CAA37732.1; -

DR EMBL; X65183; CAA46294.1; -

DR EMBL; MS5039; AAA33918.1; -

DR PIR; JQ0703; JQ0703.

DR PIR; S22519; S22519.

DR PIR; S30485; S30485.

DR PIR; JQ2224; JQ2224.

DR InterPro; IPR001296; Glycos transf_1.

DR Pfam; PF0534; Glycos transf_1; 1.

KW Glycogen biosynthesis; Transferase; Glycosyltransferase;

KW Transit peptide; Chloroplast; Starch biosynthesis.

FT TRANSIT 1 77 CHLOROPLAST.

FT CHAIN 78 609 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.

FT BINDING 97 97 UDP-GLUCOSE (BY SIMILARITY).

FT CONFLICT 247 247 N -> T (IN REF. 5).

FT CONFLICT 250 250 P -> T (IN REF. 5).

FT CONFLICT 415 415 P -> S (IN REF. 4).

SQ SEQUENCE 609 AA; 66476 MW; C225DBF6F12072C5 CRC64;

Query Match 50.5%; Score 1397.5; DB 1; Length 609;

Best Local Similarity 51.4%; Pred. No. 8.9e-87;

Matches 281; Conservative 76; Mismatches 147; Indels 43; Gaps 9;

OY 2 LDIVVAAEVPWSTGGLGVDVTGGLPIELVKGHRVMTIAPRYDQYADAMTSSVVVDI - 60

DB 83 MNVFEVGAEMAPWSTGGLGVDVLTGLGLPPAMAANGHRVWVISPRIYDKDADWTSVVAEIK 142

OY 61 ---MGEKRYEHSIKKGVHRVWIDHPWLAKVWGTGSKLYGPRSGADYLDNHKFAFLFC 117

DB 143 VADRYERVFFHCYARGVDRVFDHPSEFLEKVMWGTGKIYGPDTGVYDKNQMFSLIC 202

OY 118 KAAIFAAARVL-----PFGP---GDCVFVANDWHSALVPVLIKDEYQPKGQFTKAKSVLA 169

DB 203 QAALEAPRLNPNPFYKGYGDEVFVFCNDWHGTPGLASYLKNYQNGIYRNKAVFC 262

OY 170 IHNFAQGRMWEAFKDKLPQAAFDKLAISDGYAKVYTEATPMEEDEKPLTGTYKKI 229

DB 263 IHNISYQGRFAFEDYPELNLSERFSSEDFIDGY-----DTPVEG-----RKI 305

OY 230 NNLKGGIIAADKLVTSVPNYATEATAAAGGVELDTVIRAKGLEIYNGMIEWNPXID 289

DB 306 NNMKAGILEADRVLTSPYAEELISGTARGCEDLNMRLTGITGVNGMDVSEWDPSKD 365

OY 290 KFLSAPYDONSIVAGKAAAKALQALGLPDPPTAPLFAFIRLEQKGVDTILAAALPKI 349

DB 366 KYITAKYDATTATIAEKALNKEALQAEGLPVDKRIPLTAFIRLEEQKGVDMMAAIPEL 425

OY 350 LATPKVQIATIGTKAAVEKLVNAIGTKYGRKGVKFSAPLAHMLTAGADFMVPSRF 409

DB 426 M-QEDVQIVLLGTGKKFKELLKSMEEKYPGKVRVAVKFNAPLAHLINAGADVLAAPSRF 484

OY 410 EPCGLIQLHAMHYGTVPVWASTGGLVDYVKGSGVTFHMGALNPD--KLDEADADALATV 467

DB 485 EPCGLIQLQGMRYGTGPCASTGGLVDYVIEGKTFHMGRLSVCKVYVPSDVKKVAATL 544

OY 468 RRASEVFAGGRYPENWANCISQDLSSKPAOKWGLLEEVYVYGGK-----VATAK 518

DB 545 KRAIKVGTTPAYEEMVRNMQDLSSKPAKNWENVL--LGLGVAGSAPGTEGDEIAPLA 602

OY 519 KEETKVP 525

DB 603 KENVAAP 609

RESULT 7

UGST_HORVU STANDARD; PRT; 603 AA.

AC P09842;

DT 01-MAR-1989 (Rel. 10, Created)

DT 15-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Granule-bound glycogen [starch] synthase, chloroplast precursor (EC 2.4.1.11).

GN WAXY.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticeae; Hordeum.


```

Db 300 NMKAGILEADRLVLTSPYAEELISGARGCELDNIMRLTGITGVNMGDSEWDPGRD 359
QY 290 KFLSAPYDQNSVYAGAKAERLQAEGLPVDPTAPLFAFGRLEEQKGVDIILALPKI 349
Db 360 KYIAVKYDSTAVEAKALNKEALQAEVGLPVDNRNIPVAFGRLEEQKGVDMVMAAIPQL 419
QY 350 L-ATPKVQIATLGTGKAAYEKLVNAIGTKYKRAKGVVYKFSAPLAHMLTAGADEMLVPSR 408
Db 420 MEMVEDQIVLGLTGKKEFERMLSAEKEKFPKRAVYKFNAAALAHHIMAGADVLAITSR 479
QY 409 FEPCLLIQLHAMHYGTVPVASTGGLVDTVKEGVTFGFMGALNPD--KIDRADALAAAT 466
Db 480 FEPCLLIQLQMRXGTPCACASTGGLVDTIIEGKTGFHMGRLSDVCNVVPEADVKKVAIT 539
QY 467 VRRASEVFAGRYPPEMVANCIQSLSWSKPAQKWEGLLEE--VYVGKGV-----ATAKK 519
Db 540 LORAIKVYGTTPAYEEMVENCMIQDLSWKGPAKNENVLLSLGVAGGEPCEVEGETAPLAK 599
QY 520 EEIKVP 525
Db 600 ENVAAP 605

RESULT 12
UGS2_SOLITU STANDARD; PRT; 641 AA.
AC P93568;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Soluble glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11) (SSS)
OS Solanum tuberosum (Potato)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Desiree; TISSUE=Leaf;
RA MEDLINE=97164391; PubMed=9011082;
RX Abel G.J.W., Springer F., Willmitzer L., Kossmann J.;
RT "Cloning and functional analysis of a cDNA encoding a novel 139 kDa
RL starch synthase from potato (Solanum tuberosum L.).";
CC Plant J. 10:981-991(1996)
CC -!- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; Y10416; CAA71442.1;
CC InterPro; IPR001296; Glycos_transf_1.
CC Pfam; PF00534; Glycos_transf_1; 1.
CC Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 641 SOLUBLE GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 145 145 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 641 AA; 70608 MW; 30F8B0546CEFB74C CRC64;

Query Match 32.6%; Score 902.5; DB 1; Length 641;
Best Local Similarity 39.8%; Pred. No. 2e-53;

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Matches 212; Conservative 90; Mismatches 161; Indels 69; Gaps 19;
QY 3 DIVWAAEAPWPKTGGGLDVTGGPIELVKKRHRVMTIAPRY-----DQYADAWDRS 55
Db 132 NIIFTAEAPISKTGGDGVCGSLPMAAARGHRVWVSPRYLNGPGSDKEYANAVADLD 191
QY 56 V--VVDIMG--EKVRYFHSIKKGVHRVWIDHPWFLAKVWKGTSKLSYGRSGADYIDNHK 111
Db 192 VRATVHCFGDAQAEVAFYHEYRAGVDVWFVDDHSSYC-----RPGTP-YGDIYGA-EGDNQF 244
QY 112 REALFCKAAIEARVLPFGP---GEDCVFVANDHSHALVPVLLKDEYQKGFTRAKSVL 168
Db 245 RFTLLSHAACEAPLVPLGGFTYGEKCLFLANDWHAALVPLLLAAKYRPGYGVYKDAARSIV 304
QY 169 AIHNIAFOGRMWEAEFKDKLPQAADFKLAFSDGYAKVYVTEATPMEDEKPLTKTYKK 228
Db 305 AIHNIAHOGVEPAVYNNLGLPPQYGVAV---EWIFPTWARAHALD-----TGET--- 351
QY 229 INWLKGIITADKLVTSNPYATEIAADAAGVVELDTVI--RAKGLIEGVINGMDIEWNP 286
Db 352 VNVLKGALAVADRILTVSQYSWEITT-PEGGYGLHELLSSRSQSVINGITGIDVNDNP 410
QY 287 KTDKELSAPYDQNSVYAGAKAERLQAEGLPVDPTAPLFAFGRLEEQKGVDIILAL 346
Db 411 STDEHIASHYSTNDL-SGVQCKTDLQELGLPIRDCPLIGFIGRLDYQKGVDIILSAI 469
QY 347 PKILATPKVQIATLGTGKAAYEKLVNAIGTKYKRAKGVVYKFSAPLAHMLTAGADEMLVP 406
Db 470 PELMQN-DVQVVMGLSGKEQYEDWNRHTENLFKDFRAWGVNVPVSHRITAGCDILLMP 528
QY 407 SRFEPCLLIQLHAMHYGTVPVASTGGLVDTVVK-----EGV---TGFHMGALNPDKLD 456
Db 529 SRFEPCLLIQLYAMRYGTIPVHSTGGLRDTVKDENPYAQEGIGEGTGFSTPLTSEKL- 587
QY 457 EADADALAATVRRASEVFAAGGRYP-----MVANCIQSLSWSKPAQKWE 501
Db 588 ---LDTLKLAI-----GTYTEHKSWEGLMRGRMDRYSWENAAIQYE 627

RESULT 13
UGS2_ORYSA STANDARD; PRT; 626 AA.
AC Q40739;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Soluble glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11) (SSS)
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 114-131.
RC STRAIN=cv. Japonica; TISSUE=Seed;
RX MEDLINE=94302151; PubMed=7518089;
RA Baba T., Nishihara M., Mizuno K., Kawasaki T., Shimada H.,
RA Kobayashi E., Ohnishi S., Tanaka K.-I., Arai Y.,
RT "Identification, cDNA cloning, and gene expression of soluble starch
RT synthase in rice (Oryza sativa L.) immature seeds.";
RL Plant Physiol. 103:565-573(1993).
CC -!- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
CC -!- PATHWAY: Starch biosynthesis
CC -!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE.
CC -!- TISSUE SPECIFICITY: LEAVES AND IMMATURE SEEDS.
CC -!- MISCELLANEOUS: THREE FORMS OF SOLUBLE STARCH SYNTHASE WERE
CC PURIFIED: RSS1, RSS2 AND RSS3.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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QY 503 LLEEVVY 509
 Db 744 VLVAANKY 750

RESULT 15
 UGS2_WHEAT
 ID UGS2_WHEAT STANDARD; PRT; 610 AA.
 AC Q43654;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Soluble glycohen [starch] synthase, chloroplast precursor
 DE (EC 2.4.1.11) (Fragment).
 OS Triticum aestivum (Wheat).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 CC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. T.A. Florida; TISSUE=Endosperm;
 RA Block M., Loerz H., Luetticke S.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: UDP-glucose + [(1,4)-alpha-D-glucosyl](N) =
 CC UDP + [(1,4)-alpha-D-glucosyl](N+1).
 CC -!- PATHWAY: Starch biosynthesis.
 CC -!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
 CC FAMILY.

Search completed: June 4, 2003, 14:53:26
 Job time : 11.1299 secs

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 or send an email to license@isb-sib.ch).

EMBL: U48227; AB02197.1;
 InterPro: IPR001296; Glycos_transf_1.
 Pfam: PF00534; Glycos_transf_1; 1.
 KW Glycohen biosynthesis; Transferase; Glycosyltransferase;
 KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
 FT NON_TER 1 ?
 FT TRANSIT <1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN ? 610 SOLUBLE GLYCOGEN [STARCH] SYNTHASE.
 FT BINDING 7 7 UDP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 610 AA; 67143 MW; 46080A3B7EB87193 CRC64;

Query Match 31.3%; Score 866; DB 1; Length 610;
 Best Local Similarity 39.8%; Pred. No. 5.3e-51;
 Matches 207; Conservative 78; Mismatches 161; Indels 74; Gaps 16;

QY 10 EVAPWKTGGLGVDGGLPIELVGRHVMIAPIRY-----DQYADAWDTISVVVDIM-- 61
 Db 1 EAPYAKSGGLGVDGGLSLPTALAAARGHVMVMPRYLNGSSDKNYAKALYAKHRIKIPCF 60
 QY 62 --GEKVYFHSIKKKGVHVRWIDHPFLAKVWGTGSKLYGPRSGADYLDNHRKFALECKA 119
 Db 61 GGSHEVTFEYHRDNDVDFVDHP-----SYHRPGS-LYGDNFGA-FGDNQFRITLLCYA 113
 QY 120 ATEAARVLFGP---GEDCVFVANDHNSALVPVLLKDEYQPKQFTKAKSVLAHNIATQ 176
 Db 114 ACEAPLILLEGGYIYGQNCMFVNDHNSALVPVLLAAKVPYGVYRDSRSLVHNLAHQ 173
 QY 177 GRMWEAEFKDTLPQAAFDKAFSDGYAKVYTEATWEDEKPLTKYKKNLWLGKI 236
 Db 174 GVEPASTYDGLPPEWYGALEW-----VFPWARHRLDKG-----EAVNFKGAV 220
 QY 237 IAADKLVTSPNYATEAADAAGGVDELTVI--RAKIGIEIYNGMDIEENPKTKFLSA 294

Db 221 VTADRIVTYSQGYSEVTT-ABGGQGLNELLSSKSVLNGIVNGIDINDWNPTDKCLPH 279
 QY 295 PYDQNSVYAGKAAAEALQALGLPVDPTAPLFAFGRLEEQKGVDIILAAALPKILATPK 354
 Db 280 HYSVDDL-SGKAKCAELQKELGLPVREDVPLIGFTIGRLDYOKGIDLIKMAIPELM-RED 337
 QY 355 VOAILGTGKAAYEKLVAIGTKYGRAGVVKFSAPLAHMLTAGADEMLVPSRPPCGL 414
 Db 338 VQFVMLGSGDPIFEGRWMSRSTESSYKDKFGWVGFSVPVSHRTAGCDIILMPSRFPCCGL 397
 QY 415 IQLHAMHYGTVPVWASTGGGLVDTVK-----EGVTGFHMGALNPDKIDADADALAA 465
 Db 398 NOLYAMQYGTVPVWHGTGGLRDTVETFPNGAKGEEGTGWAFSPLTVDKMLWA----- 450
 QY 466 TVRRASEVFAGGRYPFWANCISQDLSWSKPAQKWEGLLE 505
 Db 451 -LRTAMSTFRE-----HKPS--WEGLMK 470

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 14:35:26 ; Search time 26.3807 Seconds
(without alignments)
4147.394 Million cell updates/sec

Title: US-09-980-771A-9
Perfect score: 2769
Sequence: 1 ALDIVMAAEVAPNSKTGGL.....GGVATAKKEIKVPVAKIP 531

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:.*
1: sp_archaea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phase:.*
10: sp_plant:.*
11: sp_rodent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*
15: sp_rvirus:.*
16: sp_bacteriap:.*
17: sp_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2765	99.9	708	10	064925
2	1463.5	52.9	613	10	Q93YB1
3	1450.5	52.4	604	10	Q9FR03
4	1424.5	51.4	608	10	Q93VD9
5	1423.5	51.4	606	10	Q9XIS6
6	1423.5	51.4	607	10	Q9XSQ5
7	1404	50.7	608	10	Q8VYU1
8	1397.5	50.5	609	10	Q94LY7
9	1395.5	50.4	603	10	Q8SA49
10	1390	50.2	610	10	Q9WAQ0
11	1389.5	50.2	609	10	Q8S9C4
12	1381	49.9	605	10	Q9SXX3
13	1380	49.8	605	10	Q9F0U6
14	1379	49.8	599	10	Q9SQ58
15	1376	49.7	606	10	Q43012
16	1375	49.7	604	10	Q9S7N5

17	1371	49.5	534	10	Q8W2G8
18	1369	49.4	604	10	Q9SLS6
19	1367.5	49.4	604	10	Q9SLS7
20	1367	49.4	605	10	Q9SQ51
21	1366	49.3	605	10	Q9SLS8
22	1362.5	49.2	604	10	Q9SXK4
23	1360.5	49.1	604	10	Q9SLS9
24	1354.5	48.9	605	10	Q9SQ52
25	1353.5	48.9	574	10	Q9SYU0
26	1263.5	45.6	565	10	Q9XEN9
27	898	32.4	792	10	Q9MAC8
28	895.5	32.3	313	10	Q9LKD3
29	893.5	32.3	313	10	Q9LKD3
30	893.5	32.3	313	10	Q9LKE0
31	891.5	32.2	647	10	Q9LEB9
32	891.5	32.2	647	10	Q9SQH0
33	891.5	32.2	647	10	Q9SQG9
34	890.5	32.2	647	10	Q9LECO
35	886.5	32.0	313	10	Q9LKE8
36	886	32.0	576	10	Q64926
37	885.5	32.0	313	10	Q9LKD1
38	884.5	31.9	643	10	Q9M5A3
39	879.5	31.8	313	10	Q9LKE5
40	879.5	31.8	313	10	Q9LKD6
41	878.5	31.7	313	10	Q9LKE7
42	878.5	31.7	313	10	Q9LKE1
43	877.5	31.7	313	10	Q9LKE6
44	877.5	31.7	313	10	Q9LKD8
45	876.5	31.7	313	10	Q9LKE5

ALIGNMENTS

RESULT 1

064925 PRELIMINARY; PRI; 708 AA.
AC 064925;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Granule-bound starch synthase I precursor (EC 2.4.1.21).
GN STA2.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137C;
RA D'Hulst C., Watebled F., Ral J.-P., Abel G.J., Kossmann J.,
RA Ball S.G.;
RT "Cloning of a cDNA encoding for the GBSSI in the green alga
Chlamydomonas reinhardtii.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Watebled F., Ball S.G., D'Hulst C.;
RT "Granule-bound starch synthase I: A major enzyme involved in the
biogenesis of B-crystallites in starch granules.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026420; AAC17969.3; -
DR EMBL; AF43156; AAL28128.1; -
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR002114; HPI_SerP_site.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
DR GlycoSyltransferase; Transferase; Transit peptide.
FT TRANSIT 1 57 POTENTIAL
FT CHAIN 58 708 GRANULE-BOUND STARCH SYNTHASE I.
SQ SEQUENCE 708 AA; 74623 MW; 7D2A5A07D8606469 CRC64;
Query Match 99.9% Score 2765; DB 10; Length 708;

[illegible]


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QY 61 ---MGEKVRVYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
Db 141 IGDRTETVFFHCYKKGVDVDFVDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 200
QY 118 KAAIEARVLPF-----GP-GEDCVFVANDWHSALVPLVLLKDEYQPKQFTKAKSVLA 169
Db 201 LAALAPRVLNNSSEYFSGPYGENVVFVANDWHTGVLPCYLKSIQAQGMVNAKVAFC 260
QY 170 IHNIAFOGRMWEAFKDTKLPOAFAFKLAFSDCYAKVYTEATPMEDEKPPLTGKTYKKI 229
Db 261 IHNIAFGGFAREDFELNLPDSFLPSFDFIDGHEK-----PVG-----RKI 303
QY 230 NWLKGIIAADKLVTSPNATYATIAADAAGGVLELTVIRAKGIE-GIVNGMDIEEWNPKT 288
Db 304 NWKAGITCEDLVMTVSPHYVELASGPKGVLELITKPLETGIVNGMDVYENPAT 363
QY 289 DKFELSAPYDQNSVYAGKAAKALQAEGLPVDPTAFAPFAFGRLEEQKGVDTIIAALPK 348
Db 364 DQYISVKYDATVTEARALNKEMQLQAEVGLPVDSSILPIVFGRLSEQKSDILIAAIE 423
QY 349 ILATPKVOIAILGTGKAAEKLVAIGTKYKRAKGVVVFSAPLAHMLTAGADEMLVPSR 408
Db 424 FV-EGNVQIIVLGTGKKKMEELIILEVKYPTNARGLAKFNPLAHMPFAGADFIIVPSR 482
QY 409 FEPGGLIOLHAMHYGTVPVVASTGGLVDTVKEGTVGFHMGALNP--DKLDEADADALAT 466
Db 483 FEPGGLIOLQGMRYGVVPCSTGGLVDTVKEGTVGFHMGALNPVCEVTPVDVDTAVAST 542
QY 467 VRASEVFAGRYPPEMVANCISODLSWSKPAQKWEGLLEEVYVYKGG-----GVA 515
Db 543 VKRALQYNTAFQEMVQNCMAQDLSWKGPAKKV---EEVLGLGVESQPGISGEVA 598
QY 516 TAKKEIKVP 525
Db 599 PLAKENVATP 608

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RESULT 8

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Q94LY7
ID Q84LY7 PRELIMINARY; PRT; 609 AA.
AC Q84LY7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Granule-bound starch synthase (EC 2.4.1.21).
GN WAXY
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. REMONT;
RA Larkin P.D., McClung A.M., Ayres N.M., Park W.D.;
RT "The Wx locus (Granule Bound Starch Synthase) is strongly associated
RT with pasting curve characteristics in rice (Oryza sativa L.).";
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF141954; AAF72561.1; -
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00534; Glycos_transf_1.1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
SQ SEQUENCE 609 AA; 66466 MW; 6D2615EB203CBDC8 CRC64;

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Query Match 50.5%; Score 1397.5; DB 10; Length 609;
Best Local Similarity 51.4%; Pred. No. 3.5e-87;
Matches 281; Conservative 76; Mismatches 147; Indels 43; Gaps 9;
QY 2 LDIWVAAEAVAPWSKTGGLGVDVGTGGLPIELVKRHRVMTIAPRYDQYADAMDTSVVVDI- 60
Db 83 MNVVFVGAEMAPWSKTGGLGVDVGTGGLPIELVKRHRVMTIAPRYDQYADAMDTSVVVDI- 142

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QY 61 ---MGEKVRVYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
Db 143 VADRYERVRFHCYKKGVDVDFVDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 202
QY 118 KAAIEARVLPF-----PFGP---GEDCVFVANDWHSALVPLVLLKDEYQPKQFTKAKSVLA 169
Db 203 QAALEAPRVLNNSSEYFSGPYGENVVFVANDWHTGVLPCYLKSIQAQGMVNAKVAFC 262
QY 170 IHNIAFOGRMWEAFKDTKLPOAFAFKLAFSDCYAKVYTEATPMEDEKPPLTGKTYKKI 229
Db 263 IHNISVQGFAREDFELNLPDSFLPSFDFIDGHEK-----DTPVEG-----RKI 305
QY 230 NWLKGIIAADKLVTSPNATYATIAADAAGGVLELTVIRAKGIEGIVNGMDIEEWNPKTD 289
Db 306 NWKAGITCEDLVMTVSPHYVELASGPKGVLELITKPLETGIVNGMDVSEWPSKD 365
QY 290 KFLSAPYDQNSVYAGKAAKALQAEGLPVDPTAFAPFAFGRLEEQKGVDTIIAALPKI 349
Db 366 KYITAKYDATVTEARALNKEMQLQAEVGLPVDSSILPIVFGRLSEQKSDVMAAIIPEL 425
QY 350 LATPKVOIAILGTGKAAEKLVAIGTKYKRAKGVVVFSAPLAHMLTAGADEMLVPSRF 409
Db 426 M-QEDVQIIVLGTGKKKMEELIILEVKYPTNARGLAKFNPLAHMPFAGADFIIVPSRF 484
QY 410 EPGGLIOLHAMHYGTVPVVASTGGLVDTVKEGTVGFHMGALNP--KLDEADADALATV 467
Db 485 EPGGLIOLQGMRYGTPCACASTGGLVDTVIEGTVGFHMGRLSDCKVVFSDVKKVAATL 544
QY 468 RRASEVFAGRYPPEMVANCISODLSWSKPAQKWEGLLEEVYVYKGG-----VATAK 518
Db 545 KRAIKVGVGPAYEEMVNCMDLSWKGPAKKWENVL--LGLGVAGSAPGIEGDEIAPLA 602
QY 519 KEEIKVP 525
Db 603 KENVAAP 609

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RESULT 9

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Q8SA49
ID Q8SA49 PRELIMINARY; PRT; 603 AA.
AC Q8SA49;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Granule-bound starch synthase.
GN 259116.5.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MEREK;
RA Ma J., Sanmiquel P.J., Dubcovsky J., Shiloff B.A., Rostoks N.,
RA Jiang Z., Busso C.S., Kleinhofs A., Devos K.M., Ramakrishna W.,
RA Bennetzen J.L.;
RT "Comparative sequence analysis of Wx1 homologous regions in barley,
RT maize, pearl millet, rice, sorghum and diploid wheat.";
RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF474373; AAL77109.1; -
SQ SEQUENCE 603 AA; 66280 MW; 467A3DE6A82125CB CRC64;

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Query Match 50.4%; Score 1395.5; DB 10; Length 603;
Best Local Similarity 53.3%; Pred. No. 4.7e-87;
Matches 277; Conservative 71; Mismatches 141; Indels 31; Gaps 7;
QY 2 LDIWVAAEAVAPWSKTGGLGVDVGTGGLPIELVKRHRVMTIAPRYDQYADAMDTSVVVDIM 61
Db 76 MNVVFVGAEMAPWSKTGGLGVDVGTGGLPPAMAANGHRVMTIAPRYDQYADAMDTSVISIK 135
QY 62 ---GEKVRVYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117

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Db 136 VADEYERVRFFHCYKRGVDRVFIDHPWFLEKVRKTKETKIYGPDAAGTDTYEDNQORFSLIC 195
Qy 118 KAATEARVL-----PE--GP-GRDCVVFVANDWHSALVPLVLLKDEYOPKQGTAKAKSVLA 169
Db 196 QAALEAPRIILNNPFFSGPYGDEYVVCNDWHTGLACVLYKSNYOSNGIYRTAKVAFC 255
Qy 170 IHNAFOGRMWEAFKTKLPQAFADKLAFSDGYAKVYVTEATPMEDEKPPPLTGKTYKKI 229
Db 256 IHNSYGRSFDFDAQLNLPDRKSSFDIDGYDX-----PVEG---RKI 298
Qy 230 NWLKGIIADKLVTSPNTATEITAADAAGVELDVTIRAKGIRGIVNGMDIEWPKTD 289
Db 299 NWKAGILOADKVLTVSPYAEELISGEARGCELDNIMRELTGITGIVNGMDVSEWDETKO 358
Qy 290 KELSAPYDONSAGKAAKALQALGLPVDTPAPLFAFAGTGRLEEKQGVLDIIAALPKI 349
Db 359 KFLAVNYDITITALEKALNKEALQALGLPVDTPAPLFAFAGTGRLEEKQGVLDIIAALPEI 418
Qy 350 LATPKVQITAILGTGKAAYEKLVAIGTKYKRAKGVVKSAPLAHMLTAGADFMVFSRF 409
Db 419 LKEEDVQIILGTGCKKFEKLLKSMEEKFKGVRAVVRFNAPLAHOMMAGADLLAVTSRF 478
Qy 410 EPCGLIOLHAMHYGTVPVASTGGLVDTVKEGVTGFHMGALNPD--KLDEADADALAATV 467
Db 479 EPCGLIOLQGMRYGTCPVCASTGGLVDTIVEGTGFHMGRLSVDCNVVPEADVKVATTL 538
Qy 468 RRASEVAGGRYPPEMVANCISODLSWSKPAQKWEGLLEEV 507
Db 539 KRAVKVGTGPAYQEMVNCMIQDLWSKPAKWNEDVLEL 578

RESULT 10
Q9MAQ0
ID Q9MAQ0 PRELIMINARY; PRT; 610 AA.
AC Q9MAQ0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Granule-bound starch synthase.
GN F911.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Federpiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Nguyen M., Lam B., Southwick A., Bei, Buehler E., Chin C.,
RA Chou J., Choi E., Dunn P., Gonzalez A., Howng B., Kim C., Koo T.,
RA Lee J.M., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
RA Pham P., Sakano H., Schwartz J., Shinn P., Thayeri A., Toriumi M.,
RA Vaysberg M., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006424; AAF31273.1;
DR InterPro; IPR001296; Glycosyltransf. 1.
DR Pfam; PF00534; Glycosyltransf. 1.
SQ SEQUENCE 610 AA; 66879 MW; CF17F25BE12220DF CRC64;

Query Match 50.2%; Score 1390; DB 10; Length 610;
Best Local Similarity 52.7%; Pred. No. 1.1e-86;
Matches 287; Conservative 72; Mismatches 146; Indels 40; Gaps 12;
Qy 2 LDIVMVAEAVPWSKTGGLGVDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI- 60
Db 84 MSVIFIGAVGWSKTGGLGVDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVQIK 143
Qy 61 MGEK---VRYFHSIKKGVHRVWIDHPFLAKVWGKSGKLYGPRSGADYLDNKHKRALFC 117
Db 144 VGDKVENVRFFHCYKRGVDRVFDHPFLAKVWGKSGKLYGPRSGADYLDNKHKRALFC 203
Qy 118 KAATEARVLPE-----GP-GRDCVVFVANDWHSALVPLVLLKDEYOPKQGTAKAKSVLA 169

Db 204 QAALEAPQVLNLSKSYFSGPYGDEYVVCNDWHTGLACVLYKSNYOSNGIYRTAKVAFC 263
Qy 170 IHNAFOGRMWEAFKTKLP---QAAFDKLAFLSDGYAKVYVTEATPMEDEKPPPLTGKTY 226
Db 264 IHNAFOGRMWEAFKTKLP---QAAFDKLAFLSDGYAKVYVTEATPMEDEKPPPLTGKTY 303
Qy 227 KKNLKGIIADKLVTSPNTATEITAADAAGVELDVTIRAKGIRGIVNGMDIEWPKTD 286
Db 304 RKNMKAALAEHRVLTSPYAEELISGEARGCELDNIMRELTGITGIVNGMDVSEWDETKO 363
Qy 287 KTFKLSAPYDONSAGKAAKALQALGLPVDTPAPLFAFAGTGRLEEKQGVLDIIAAL 346
Db 364 STDYIDIKYDITITALEKALNKEALQALGLPVDTPAPLFAFAGTGRLEEKQGVLDIIAAL 423
Qy 347 PKLATPKVQITAILGTGKAAYEKLVAIGTKYKRAKGVVKSAPLAHMLTAGADFMVFSRF 406
Db 424 SKFMGL-NVQMVILGTGCKKFEKLLKSMEEKFKGVRAVVRFNAPLAHOMMAGADLLAVTSRF 482
Qy 407 SRFEPCGLIOLHAMHYGTVPVASTGGLVDTVKEGVTGFHMGALNPD--DKLDEADADALA 464
Db 483 SRFEPCGLIOLHAMHYGTVPVASTGGLVDTVKEGVTGFHMGALNPD--DKLDEADADALA 542
Qy 465 ATVRASEVAGGRYPPEMVANCISODLSWSKPAQKWEGLLEEVYKGVATAKKEELKV 524
Db 543 KAVTRAVAVYGTSAQEMVNCMIQDLWSKPAKWNEDVLEL 600
Qy 525 PVAEK 529
Db 601 PLAKE 605

RESULT 11
Q8S9C4
ID Q8S9C4 PRELIMINARY; PRT; 609 AA.
AC Q8S9C4;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Starch granule-bound starch synthase.
GN WX-1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MILKY QUEEN;
RA Sato H., Suzuki Y., Sakai M., Imbe T.,
RT "Molecular Characterization of wx-1, a Novel Mutant Gene for Low-
amylose Content in Endosperm of Rice (Oryza sativa L.).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB066093; BAB88209.1;
SQ SEQUENCE 609 AA; 66431 MW; B57CC13E040D227 CRC64;

Query Match 50.2%; Score 1389.5; DB 10; Length 609;
Best Local Similarity 51.2%; Pred. No. 1.2e-86;
Matches 280; Conservative 76; Mismatches 148; Indels 43; Gaps 9;
Qy 2 LDIVMVAEAVPWSKTGGLGVDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI- 60
Db 83 MNVVFVGAEMAPWSKTGGLGVDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVAEK 142
Qy 61 ---MGEKVRYFHSIKKGVHRVWIDHPFLAKVWGKSGKLYGPRSGADYLDNKHKRALFC 117
Db 143 VADRYERVRFFHCYKRGVDRVFDHPFLAKVWGKSGKLYGPRSGADYLDNKHKRALFC 202
Qy 118 KAATEARVLPE-----PFGP---GDCVVFVANDWHSALVPLVLLKDEYOPKQGTAKAKSVLA 169
Db 203 QAALEAPRIILNNPFFSGPYGDEYVVCNDWHTGLACVLYKSNYOSNGIYRTAKVAFC 262
Qy 170 IHNAFOGRMWEAFKTKLPQAFADKLAFSDGYAKVYVTEATPMEDEKPPPLTGKTYKKI 229


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Db 263 IHNISYQGRFADPELNLSEFRSSDF IDGY -----DTPVEG-----RKI 305
QY 230 NWLKGITTAADKLVTVSPNYATEIAADAAGGVLDIVIRAKGIEGIVNGMDIEEWNPKTD 289
Db 306 NMWAGILEADRVLTVPSPYAEELISGTARGCELDINMLRTGITGIVNGMDVSEWDPSKD 365
QY 290 KFLSAPYDONSVIYAGKAAKEALQAEGLPLVDPTAPLFAFGRLEEQKGVDIILALPKI 349
Db 366 KYITAKYDATTAEIAKALKALQAEGLPVDKIPLFAFGRLEEQKGVDPVMAAIAPEL 425
QY 350 LATPKVQIALLGTGKAAEYKLVNAICTYKGRAGKGVKFSAPLAHMLTAGADMELVPSRF 409
Db 426 M-QEDVQIVLLGTGKKEKELLSMEKYPGKVRVAVKFNAPLAHLIMAGADVLAVERF 484
QY 410 EPCGLIQLHAMHYGTVPVASTGGGLVDIVKGVTFGHMGALNPD--KLDEADADALAATV 467
Db 485 EPCGLIQLQGRYGTTPCACASTGGGLVDIVIEGKTGFHMGRLSVDCCKVVEPSDVKKVAATL 544
QY 468 RRASEVFAGGRYPPEMVANCISQDLSWSKPAOKWEGLEEVYVYGRGG-----VATAK 518
Db 545 KRAIKVVGTPAYEEMVRNQMQLSWKGPARNWNLV--LGLGVAGSAPGIEGDEIAPLA 602
QY 519 KEEIKVP 525
Db 603 KENVAAP 609

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RESULT 12

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Q9SXX3 ID Q9SXX3 PRELIMINARY; PRT; 605 AA.
AC Q9SXX3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Starch synthase (GBSSI) (EC 2.4.1.21).
GN WAXY.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99321800; PubMed=10393240;
RA Murai J., Taira T., Ohta D.;
RT "Isolation and characterization of the three Waxy genes encoding the
RT granule-bound starch synthase in hexaploid wheat.";
RL Gene 234:71-79(1999).
DR EMBL; AB019623; BAA77351.1; -.
DR InterPro; IPR001296; Glycosyl-transf_1.
DR Pfam; PF00534; Glycosyl-transf_1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR Glycosyltransferase; Transferase.
SQ SEQUENCE 605 AA; 66345 MW; 60A816276F78722B CRC64;

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Query Match 49.9%; Score 1381; DB 10; Length 605;
Best Local Similarity 51.5%; Pred. No. 4.6e-86;
Matches 281; Conservative 72; Mismatches 153; Indels 40; Gaps 9;
QY 2 LDIWMAAEVAPWSKTGGLGVDTGGLPIELVKGRHVMVTAIPRYDQYADAWDTSVVVDIM 61
Db 78 MNLVFCGAEMAPWSKTGGLGVDTGGLPPAAMANGHRVMVISPRTDQYKDAWDTSVVSEIK 137
QY 62 ----GEKVRVFHSIKGVRHWIDHPWFLAKVWGKTSKLYGPRSGADYLDNIHKKRFLFC 117
Db 138 VADEYERVRVFCYKRGVDRVFDHPCFLKVRGKTKYKIGPDAGTDYEDNQLRFLSLLC 197
QY 118 KAAIEARVL-----PF--GP-GEDEVFVANDHMSALVPVLLKDEYQPKGQFTAKSVLA 169
Db 198 QAALEAPRIILNNPNYFSGPYGDEVVVCNDWHTGLLACYLKSNGYSSGIYRTAKVAF 257

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QY 170 IHNIAFQGRMBEAFKDTKLPOAAFDKLAESDGIYAKVYTEATPMEDEKEPPLTGKTYKKI 229
Db 258 IHNISYQGRFSEDDFAQLNLPDRFKSSDF IDGYDK-----PVES-----RKI 300
QY 230 NWLKGITTAADKLVTVSPNYATEIAADAAGGVLDIVIRAKGIEGIVNGMDIEEWNPKTD 289
Db 301 NMWAGILEADRVLTVPSPYAEELISGEARGCELDINMLRTGITGIVNGMDVSEWDPAKD 360
QY 290 KFLSAPYDONSVIYAGKAAKEALQAEGLPLVDPTAPLFAFGRLEEQKGVDIILALPKI 349
Db 361 KFLAANYDVTTALECKALKALQAEGLPVDKIPLFAFGRLEEQKGVDPVMAAIAPEI 420
QY 350 LATPKVQIALLGTGKAAEYKLVNAICTYKGRAGKGVKFSAPLAHMLTAGADMELVPSRF 409
Db 421 LKEEDVQIVLLGTGKKEKELLSVEKFPKVRVAVKFNAPLAHMQMAGADVLAVERF 480
QY 410 EPCGLIQLHAMHYGTVPVASTGGGLVDIVKGVTFGHMGALNPD--KLDEADADALAATV 467
Db 481 EPCGLIQLQGRYGTTPCACASTGGGLVDITMEGKTGFHMGRLSVDCNVVEPADVKVVTTL 540
QY 468 RRASEVFAGGRYPPEMVANCISQDLSWSKPAOKWEGLEEV-----VYKGGVATAKK 519
Db 541 KRAIKVVGTPAYEEMVRNQMQLSWKGPARNWNLV--LGLGVAGSAPGIEGDEIAPLA 599
QY 520 KEEIKVP 525
Db 600 ENVAAP 605

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RESULT 13

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Q9FUU6 ID Q9FUU6 PRELIMINARY; PRT; 605 AA.
AC Q9FUU6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Granule bound starch synthase I (EC 2.4.1.21).
GN GBSSI.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. CHEYENNE; TISSUE=ENDOSPERM;
RA McCue K.F., Hurkman W.J., Tanaka C.K., Anderson O.D.;
RT "Starch Branching Enzymes Sbel and Sbe2 from Wheat (Triticum aestivum
RT cv. Cheyenne): Molecular Characterization, Developmental Expression,
RT and Homolog Assignment by Differential PCR.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286320; AAG27624.1; -.
DR InterPro; IPR001296; Glycosyl-transf_1.
DR Pfam; PF00534; Glycosyl-transf_1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR Glycosyltransferase; Transferase.
SQ SEQUENCE 605 AA; 66326 MW; 21120D9D6F68B891 CRC64;

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Query Match 49.8%; Score 1380; DB 10; Length 605;
Best Local Similarity 51.5%; Pred. No. 5.4e-86;
Matches 281; Conservative 72; Mismatches 153; Indels 40; Gaps 9;
QY 2 LDIWMAAEVAPWSKTGGLGVDTGGLPIELVKGRHVMVTAIPRYDQYADAWDTSVVVDIM 61
Db 78 MNLVFCGAEMAPWSKTGGLGVDTGGLPPAAMANGHRVMVISPRTDQYKDAWDTSVVSEIK 137
QY 62 ----GEKVRVFHSIKGVRHWIDHPWFLAKVWGKTSKLYGPRSGADYLDNIHKKRFLFC 117
Db 138 VADEYERVRVFCYKRGVDRVFDHPCFLKVRGKTKYKIGPDAGTDYEDNQLRFLSLLC 197
QY 118 KAAIEARVL-----PF--GP-GEDEVFVANDHMSALVPVLLKDEYQPKGQFTAKSVLA 169

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Db 198 QAALAPRILDLNNPFGSPGYGEDVVFVVCNDWHTGILLACYLKSQSYRTAKVAF 257
QY 170 IHNIAPQGRMWEAFKDTKLPOAFAFKLAFSDGYAKVYTEATPMEDEKPLTKYTKI 229
Db 258 IHNISYQGRSFDDFAQLNLPDRFKSDFDIDYDK-----PVGE---RKI 300
QY 230 NWLKGIIAADKLVTSYSPNATEIAADAAGVELDTVIRAKGTGIVNGMDIEBWNPKTD 289
Db 301 NWKAGILQADKLVTSYSPNATEIAADAAGVELDTVIRAKGTGIVNGMDIEBWNPKTD 360
QY 290 KFLSAPYDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFIFGRLEQKGVDIILAAAPKI 349
Db 361 KFLAANYDVTVALEGRALNKEALQAEVGLPVDKRVPLVAFITGRLEQKGVDMIAALPEI 420
QY 350 LATPKVQIATILGTGKAAEKLVAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPSRF 409
Db 421 LKEDVQIVLIGTGKKEFLKLSVEEKFSSKRVAVVRFNAPLAHQMGADGVLAVTSRF 480
QY 410 EPCGLIQLHAMHYGTVPVAVASTGGLVDTVKEGTVGFHMGALNP--KLDEADADALAATY 467
Db 481 EPCGLIQLQMGRYGTCCACASTGGLVDTIMEGKTGFHMGHLSVDCNVVPEADVKVVTIL 540
QY 468 RRASEVPAGRYPEMVANCIQSOLSWKSPAKKWEGLLEEV-----VYKGGVATAKK 519
Db 541 KRAVKVVGTPAYHEMVKNCMIQDLSWKGPAKNWEDVILLEGVGESEPGVIGE-BIAPLAM 599
QY 520 EEIKVP 525
Db 600 ENVAAP 605

RESULT 14
Q9SQ58 PRELIMINARY: PRT; 599 AA.
AC Q9SQ58;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Granule-bound starch synthase GBSSII.
OS Triticum aestivum (Wheat)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakamura T., Vrinten P.; to the EMBL/GenBank/DBJ databases.
RL EMBL; AF109395; AAF14233.1; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
SQ SEQUENCE 599 AA; 66045 MW; D486EFC90557F131 CRC64;

Query Match 49.8%; Score 1379; DB 10; Length 599;
Best Local Similarity 50.4%; Pred. No. 6.3e-86;
Matches 277; Conservative 78; Mismatches 147; Indels 48; Gaps 10;

QY 2 LDIYVVAEAVAPWSKTGGTGLGVDTGGLPIELVKGHRVMTIAPRYDQYADAWDTSVVVDIM 61
Db 72 MPILFTEVHPWCKTGGTGLGVDTGGLPVALAAMGHRVMTIAPRYDQYKDTWDTNVLVEVI 131
QY 62 ---GEKVRYPHSTKKGVRHWIDHPWFLAKVWGKTGSKLGPSCADYLNNHKKFALPC 117
Db 132 VGDRTETVRFFHCYKRGVDRVDFHPMELEKVGWKTGSKLGPPTGTDFRONQLRFLC 191
QY 118 KAAIEAARVLPF-----GP-GEDEVFANDWHSALVPLVLLKDEYQKQFTKAKSVLA 169
Db 192 LAALAPRVNLNNSEYSGPYGENVFEVANDWHTAVLPCLYKSMYKONGIYVNAKAVPC 251
QY 170 IHNIAPQGRMWEAFKDTKLPOAFAFKLAFSDGYAKVYTEATPMEDEKPLTKYTKI 229
Db 252 IHNIAPQGRFPVDFEILLNLPESFMPDFDVGHVK-----PVVG---RKI 294

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QY 230 NWLKGIIAADKLVTSYSPNATEIAADAAGVELDTVIRAKGTGIVNGMDIEBWNPKT 288
Db 295 NWKAGITCEDVLTIVTSYSPNATEIAADAAGVELDTVIRAKGTGIVNGMDIEBWNPKT 354
QY 289 DKFLSAPYDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFIFGRLEQKGVDIILAAAPK 348
Db 355 DKYTSVKNATVAEARALNKEILQAEVGLPVDSSIPVIFIGRLEQKGVDIILAAAPK 414
QY 349 ILATPKVQIATILGTGKAAEKLVAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPSR 408
Db 415 FL-BENVQIIVLGTGKKEFLKLSVEEKFSSKRVAVVRFNAPLAHQMGADGVLAVTSR 473
QY 409 FEPGLIQLHAMHYGTVPVAVASTGGLVDTVKEGTVGFHMGALNP--KLDEADADALAAT 466
Db 474 FEPGLIQLQMGRYGTCCACASTGGLVDTIMEGKTGFHMGHLSVDCNVVPEADVKVVTIL 533
QY 467 VRASEVPAGRYPEMVANCIQSOLSWKSPAKKWEGLLEEVYVYKGG-----GVA 515
Db 534 VTRALKQKTPSFHAMVONCMQDLSWKGPAKNW-----EALLGLGVGSGQPIEGEIEA 589
QY 516 TAKKEEIKVP 525
Db 590 PLAKQNVATP 599

RESULT 15
Q43012 PRELIMINARY: PRT; 606 AA.
AC Q43012;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Starch granule-bound starch synthase (EC 2.4.1.11).
GN WAXY.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Z.Y., Zheng F.Q., Gao J.P., Wang X.C., Wu M., Zhang J.L.,
RA Hong M.M.;
RT *Identification of two transposon-like elements in rice Wx gene.*;
RL Sci. China B 37:437-447(1994).
DR EMBL; X64108; CAA45472.1; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR Glycosyltransferase; Transferase.
SQ SEQUENCE 606 AA; 66323 MW; E1157468A5553CE CRC64;

Query Match 49.7%; Score 1376; DB 10; Length 606;
Best Local Similarity 50.7%; Pred. No. 1e-85;
Matches 277; Conservative 77; Mismatches 148; Indels 44; Gaps 10;

QY 2 LDIYVVAEAVAPWSKTGGTGLGVDTGGLPIELVKGHRVMTIAPRYDQYADAWDTSVVVDI- 60
Db 83 MNVVFVGAEMAPWSKTGGTGLGVDTGGLPVALAAMGHRVMTISPRYDQYKADWDTSVVAEIK 142
QY 61 ---MGEKVRYPHSTKKGVRHWIDHPWFLAKVWGKTGSKLGPSCADYLNNHKKFALPC 117
Db 143 VADRTETVRFFHCYKRGVDRVDFIDHPSFLEKYGWKTGSKLGPPTGTDFRONQLRFLC 202
QY 118 KAAIEAARVLPF-----PFGP-GEDEVFANDWHSALVPLVLLKDEYQKQFTKAKSVLA 169
Db 203 Q---EAPRLNINNNPYFGTGTGDDVVFVNCNDWHTGTLPLSYLKNYKNGIYVNAKAVPC 259
QY 170 IHNIAPQGRMWEAFKDTKLPOAFAFKLAFSDGYAKVYTEATPMEDEKPLTKYTKI 229
Db 260 IHNISYQGRFAEDYPELNLSEKSSDFIDGY-----DTPVEG-----RKI 302

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QY 230 NWLKGIIADKLVTSVSPNYAIEIAADAGGVVELDTVIRAKCIEGIVNGMDIEEWNPKTD 289
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Db 303 NWMKAGIIIESDRVLTVPYIAEELISGARGCELDNIMRLTGITGIVNGMDYSEWDPSKD 362
|:| |:| :|:|:|:| |:| :|:| |:| |:| |:| |:| |:| |:| |:|
QY 290 KFLSAPYDONSYYAGKAAAEALQAEGLPVDPTAPLFAFTGRLEEOQGVDIILAAALPKI 349
|:| |:| :|:|:|:| |:| :|:| |:| |:| |:| |:| |:| |:| |:|
Db 363 KYITTKYDATTAEAKALKEALQAEAGLPVDRKVPLIAFGRLEEOQGVDMWAAAIPEL 422
|:| |:| :|:|:|:| |:| :|:| |:| |:| |:| |:| |:| |:| |:|
QY 350 LATPKVQITAILGTGKAAEKLVAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVPSRF 409
|:| |:| :|:|:|:| |:| :|:| |:| |:| |:| |:| |:| |:| |:|
Db 423 M-QENVQIVLLGTGKKFKEKLLKSMEEKYPGKVRVAVKFNAPLAHLIMAGADVLAVPSRF 481
|:| |:| :|:|:|:| |:| :|:| |:| |:| |:| |:| |:| |:| |:|
QY 410 EPCGLIOLHAMHYGTVPVWVASTGGLVDTVKEGVTGFHMGALNPD--KLDEADADALAATV 467
|:| |:| :|:|:|:| |:| :|:| |:| |:| |:| |:| |:| |:| |:|
Db 482 EPCGLIQLQGMRYGTGACASTGGGLVDTVIEGKTGFHMGRLSVDCKVVEPSDVQKVATTL 541
|:| |:| :|:|:|:| |:| :|:| |:| |:| |:| |:| |:| |:| |:|
QY 468 RRASEVFAGGRYPENMVANCISQDLSSWSPKPAQKWEGLL-----EEVVYKGGVATAKK 519
|:| |:| :|:|:|:| |:| :|:| |:| |:| |:| |:| |:| |:| |:|
Db 542 KRAIKIVGTPAYNEMVRNMCNQDLSWKGPAPKKNWENVLLGLGVAGSEPGVEGE-ETAPLAK 600
|:| |:| :|:|:|:| |:| :|:| |:| |:| |:| |:| |:| |:| |:|
QY 520 EEIKVP 525
|:| |:| :|:|:|:| |:| :|:| |:| |:| |:| |:| |:| |:| |:|
Db 601 ENVAAP 606
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Search completed: June 4, 2003, 14:56:10
Job time : 30.3807 secs

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OM protein - protein search, using sw model

Run on: June 4, 2003, 14:49:26 ; Search time 9.44713 Seconds
(without alignments)
1653.790 Million cell updates/sec

Title: US-09-980-771A-9
Perfect score: 2769
Sequence: 1 ALDIWVAEAPVWPKTGGT.....GGVATAKKEIKVPAEKIP 531

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1397.5	50.5	609	3	US-08-941-445A-7	Sequence 7, Appli
2	1360.5	49.1	600	4	US-09-388-743-22	Sequence 22, Appl
3	1353.5	48.9	533	3	US-08-941-445A-5	Sequence 5, Appli
4	1342.5	48.5	616	4	US-09-388-743-14	Sequence 14, Appl
5	1315	47.5	614	4	US-09-388-743-18	Sequence 18, Appl
6	1314.5	47.5	615	4	US-09-388-743-2	Sequence 2, Appli
7	902.5	32.6	641	4	US-08-836-567-10	Sequence 10, Appl
8	882.5	31.9	649	4	US-09-192-909-2	Sequence 2, Appli
9	878	31.7	671	4	US-09-196-390-2	Sequence 2, Appli
10	873	31.5	801	4	US-09-388-743-26	Sequence 26, Appl
11	871	31.5	767	4	US-08-836-567-8	Sequence 8, Appli
12	861.5	31.1	539	3	US-08-941-445A-21	Sequence 21, Appl
13	861.5	31.1	583	3	US-08-941-445A-13	Sequence 13, Appl
14	858	31.0	690	4	US-09-388-743-6	Sequence 6, Appli
15	845	30.5	558	4	US-08-836-567-6	Sequence 6, Appli
16	841	30.4	799	4	US-09-196-390-6	Sequence 6, Appli
17	837	30.2	698	3	US-08-941-445A-11	Sequence 11, Appl
18	726	26.2	459	4	US-08-836-567-4	Sequence 4, Appli
19	701.5	25.3	669	3	US-08-941-445A-9	Sequence 9, Appli
20	580	20.9	477	1	US-07-735-065-2	Sequence 2, Appli
21	580	20.9	477	1	US-08-469-202-12	Sequence 12, Appl
22	580	20.9	477	2	US-08-484-434C-12	Sequence 12, Appl
23	568.5	20.5	677	4	US-08-836-567-2	Sequence 2, Appli
24	568.5	20.5	1197	4	US-08-836-567-12	Sequence 12, Appl
25	568.5	20.5	1230	2	US-08-968-542C-35	Sequence 35, Appl
26	545	19.7	735	4	US-09-115-704-2	Sequence 2, Appli
27	530.5	19.2	533	4	US-09-388-743-10	Sequence 10, Appl

28	504	18.2	1674	2	US-08-968-542C-12	Sequence 12, Appli
29	240	8.7	64	2	US-08-470-720-15	Sequence 15, Appl
30	215.5	7.8	79	2	US-08-470-720-13	Sequence 13, Appl
31	143.5	5.2	59	2	US-08-470-720-14	Sequence 14, Appl
32	129	4.7	30	2	US-08-470-720-9	Sequence 9, Appli
33	122	4.4	29	2	US-08-470-720-16	Sequence 16, Appli
34	121	4.4	27	2	US-08-470-720-7	Sequence 7, Appli
35	112	4.0	34	2	US-08-470-720-11	Sequence 11, Appl
36	112	4.0	1037	4	US-09-134-001C-4794	Sequence 4794, Ap
37	108	3.9	701	4	US-09-132-028-2	Sequence 2, Appli
38	107	3.9	69	2	US-08-470-720-6	Sequence 6, Appli
39	107	3.9	111	2	US-08-470-720-18	Sequence 18, Appl
40	105.5	3.8	490	4	US-09-292-225-41	Sequence 41, Appl
41	105.5	3.8	509	4	US-09-292-225-35	Sequence 35, Appl
42	105.5	3.8	509	4	US-09-292-225-38	Sequence 38, Appl
43	104.5	3.8	387	4	US-09-134-001C-3206	Sequence 3206, Ap
44	104	3.8	722	4	US-09-134-001C-5482	Sequence 5482, Ap
45	104	3.8	807	4	US-08-855-910-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-941-445A-7
; Sequence 7, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-941-445A-7

Query Match 50.5%; Score 1397.5; DB 3; Length 609;
Best Local Similarity 51.4%; Pred. No. 6.7e-134;
Matches 281; Conservative 76; Mismatches 147; Indels 43; Gaps 9;
QY 2 LDIVWVAEAPVWPKTGGTGLGVTLAPRYDQYADAMDTSVVYDI- 60
Db 83 MNVVFVGAEMAPWSKTKGLGLVLPMAANGHRVWVWISPRYDQYKDAWDTSVVAEIK 142

QY 61 ---MGEKVFYHSIKKGVHVRWIDHPWELAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
DB 143 VADRYERVRFFHCYKRGVDKRVFIDHSEFLKVGKTKGKIYGPDTGVYKQDNQRRSLLC 202
QY 118 KAAATEARVL-----PFGP---GEDCVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVLA 169
DB 203 QAAALEAPRIILNANNPYFKGTGVEDVVCNDWHTGTLASLYLKNNTOPNGIYRNAKAVFC 262
QY 170 IHNIAFGGRWEAFKDTKLPQAAFDKLAESDGYAKVYVTEATPMEDEKEPPLTGKTYKKI 229
DB 263 IHNISYQGRFAFEDYELNLSERFRSFDIDGY-----DTPVEG-----RKI 305
QY 230 NWLKGIIADKLVTVSPNATETAADAAGGVELDTVIRAKGIEGIVNGMDIEBWNPKTD 289
DB 306 NWMKAGILEADRVLTVPYAEELISGIARGCELDNIMRLTGITGIVNGMDVSEWDSKD 365
QY 290 KFLSAPYDQNSVYAGKAAAEALQAEGLPVDTPAPLFAFIRLEEGKGVDIILAAALPKI 349
DB 366 KYITAKYDATTATEAKALKEALQAEAGLPVDRKRIPLIAFIRLEEGKGVDPVMAAALPEL 425
QY 350 LATPKVQIAILGTGKAAYEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMIVPSRF 409
DB 426 M-QEDVQIVLGTGKKEFKLLSMEEEKYPCKVAVVVKFNAPLAHLIMAGADVLAIVPSRF 484
QY 410 EPCGLIQHMHYGTVPVWASTGGLVDTVKEGTVGFHMGALNPD--KLDEADADALAATV 467
DB 485 EPCGLIQHMHYGTVPVWASTGGLVDTVKEGTVGFHMGALNPD--KLDEADADALAATV 544
QY 468 RRASEVFAAGGRYPPEMVAANCISQDLSWSKPAQKWEGLEEVVYKGG-----VATAK 518
DB 545 KRALKVYGTPAYEDMVRNMCNQDLSWKGPAKNWENVL--LGLGVAGSAPGTGDEIAPLA 602
QY 519 KEEIKVP 525
DB 603 KENVAAP 609

RESULT 2
US-09-388-743-22
; Sequence 22, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Ian
; TITLE OF INVENTION: No. 6423886el Starch Synthese Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Tulipa fosteriana
US-09-388-743-22

Query Match 49.1%; Score 1360.5; DB 4; Length 600;
Best Local Similarity 49.9%; Pred. No. 4e-130;
Matches 272; Conservative 77; Mismatches 157; Indels 39; Gaps 9;

QY 2 LDIVMVAEAVPWSKGTGLGVDGTGGLPIELVKRHRVMTIAPRYDQYADAWPTSVVVDI- 60
DB 73 MNLVFGTGTGYSYKGTGLGVDGVLGPPALAAARGHRVMVTPRYDQYKDAWNTVLEIK 132
QY 61 MEEK---VRYFHSIKKGVHVRWIDHPWELAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
DB 133 VGDKNMVTFRFFLHRKGRVDRVFDHPWELAKVWGKTSKLYGPRSGADYLDNHRKRALFC 192
QY 118 KAAATEARVL-----GP-GEDCVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVLA 169
DB 193 QAAALEAPRIILNNSKYFSGPYGEDVVFVANDWHTGTLASLYLKNNTOPNGIYRNAKAVFC 252

QY 170 IHNIAFGGRWEAFKDTKLPQAAFDKLAESDGYAKVYVTEATPMEDEKEPPLTGKTYKKI 229
DB 253 IHNMAYGGRFAFEDYELNLSERFRSFDIDGY-----DTPVEG-----RKI 295
QY 230 NWLKGIIADKLVTVSPNATETAADAAGGVELDTVIRAKGIEGIVNGMDIEBWNPKTD 289
DB 296 NWMKAGILEADRVLTVPYAEELISGIARGCELDNIMRLTGITGIVNGMDVSEWDSKD 355
QY 290 KFLSAPYDQNSVYAGKAAAEALQAEGLPVDTPAPLFAFIRLEEGKGVDIILAAALPKI 349
DB 356 KFIITANDATMTVEAKRNKQELQAEGLPVDTPVIVFVGRLEEGKGSILAAALPEL 415
QY 350 LATPKVQIAILGTGKAAYEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMIVPSRF 409
DB 416 M-DENVQIILGTGKKELEETEFQFDPKMLVAKFNVPFLAHMMAGGDFIIPSRF 474
QY 410 EPCGLIQHMHYGTVPVWASTGGLVDTVKEGTVGFHMGALNPD--KLDEADADALAATV 467
DB 475 EPCGLIQHMHYGTVPVWASTGGLVDTVKEGTVGFHMGALNPD--KLDEADADALAATV 534
QY 468 RRASEVFAAGGRYPPEMVAANCISQDLSWSKPAQKWEGLEEVVYKGGVATAKE 520
DB 535 KRALKVYGTPAYEDMVRNMCNQDLSWKGPAKNWENVL--LGLGVAGSAPGTGDEIAPLA 594
QY 521 EIKVP 525
DB 595 NVAAP 599

RESULT 3
US-08-941-445A-5
; Sequence 5, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 533 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-941-445A-5

[illegible]

RESULT 5
US-09-388-743-18
; Sequence 18, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:

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: TITLE: ZHOU, Lan
: TITLE OF INVENTION: No. 6423886el starch Synthase Polynucleotides and Their
: FILE OF INVENTION: Use in the Production of New Starches
: FILE REFERENCE: 1144
: CURRENT APPLICATION NUMBER: US/09/388,743
: CURRENT FILING DATE: 1999-09-02
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 18
: LENGTH: 614
: TYPE: PRT
: ORGANISM: Typha latifolia
: US-09-388-743-18

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88	MDLVFVGAEAFWWSKTKGGGLDVLGGGLPPALAAANGHRVMVTPADYDGYMDANDTDAVLVK	147
QY	MG----	61
DB	EVRYFHSIKKGVHRVTHDPWFLAKVWGKTKGSKLYGRPSGADYLDNHKRRALFC	117
DB	VDGRCETVRFVHCYKRGVDKVFVDHPMFLAKVWGKTKGKLYGPTGTDYQDNLRFSLC	207
QY	KAATIAEARVLPF-----	118
DB	CP-GEDCVFVANDWHSALVPVLLKDEYQPKQFTAKSVLA	169
DB	QAALRAPRLINNSDSFGPYGDEVFICTNDWHTSLIFCYLTKSMYHPRGYIKNAKVAFC	267

QY 170 IHNIAPQGRMEAEAFKDKLPQAAFDKLAFLSDGYAKVYVTEATPMEDEKPPILTKYKKI 229
Db 268 IHNISQGRFSDFEFLNLPENFKSFSFIDGYNK-----PVKG---MKI 310
QY 230 NMLKGGIIAADKLIVTSPNYATEIAADAAGGVDELTVIRAKGLEGVINGMDIEWPKID 289
Db 311 NNMKAGILESDRVFTVSPYQAQLLSGEERGVDELNLRVTSTITGVINGMDVNEWPNLTD 370
QY 290 KFLSAPYDONSIVYAGKAAKEALQALGLPVDPTAPLFAFICGRLEKQGVDIILALPKI 349
Db 371 KYLSVNDKAPVMEAKPLNKEALQALGLPVDPTAPLFAFICGRLEKQGVDIILALPKI 430
QY 350 LAPPKVOIALTGKAAEKLVAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVPSRF 409
Db 431 M-DENVQLIILGTGKKEMENQLESMEEMFDPKVRVNMKFNAPLAHQMTAGADIIVIPSRF 489
QY 410 EPCGLIQLHAMHYGTVPVAVASTGGLVDTVKEGVTGFMHGAALNP--DKLDEADADALAATV 467
Db 490 EPCGLIQLQCMQYGTFSACSSSTGGLVDTVKEGVTGFMHGFSAFCEVVDLSLVKKVVITY 549
QY 468 RRASEVPAGGRYPPEMVAVANCISODLSWSKPAQKWEGLL-----EENVYKGGVATAK 523
Db 550 KRALKVGTGTPAFEMTQNCMAQDLSWKGPAKNEQVLLNL-----GVAGSEPGYDGEI- 603
QY 524 VPVAEK 529
Db 604 VPLAKE 609

RESULT 6
US-09-388-743-2
; Sequence 2, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886a1 Starch Synthase Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; NUMBER FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Curcuma zedoaria
US-09-388-743-2

Query Match 47.5%; Score 1314.5; DB 4; Length 615;
Best Local Similarity 49.5%; Pred. No. 2.1e-125;
Matches 271; Conservative 76; Mismatches 157; Indels 43; Gaps 12;
QY 2 LDIVWVAEVPWSKGTGLGDTGGLPIELVKRHRVMTIAPRYDQYADAWTTSVVVDI- 60
Db 89 MNLIFVAEVPWSKGTGLGDTGGLPIELVKRHRVMTIAPRYDQYADAWTTSVVVDI- 148
QY 61 MG---EKVRYTHS IKKGVHRYWIDHPFLAKVWGTGSKLYGPRSGADYLDNHRKRFALFC 117
Db 149 VGDRIETVRFHCYKRGVDRVFDPLFLEKVGWGTGGKIYGPVTVTDYEDNQLRCLLC 208
QY 118 KAAIEAARYL-----PFGP-GEDCVFVNDWHSALVPVLKLD-EYQPKGQFTAKSVL 168
Db 209 LATLETPTVPLNPNNNKHYSGPKGED-LETANDWHTALLPCYLKTTIVYQAHGYKNAKAVF 267
QY 169 AHNHAFQGRWEEAFKDKLPQAAFDKLAFLSDGYAKVYVTEATPMEDEKPPILTKYKKI 228
Db 268 CIHNAYQGRFAFEDFSRLNLPDFTKSFDFIDGYAK-----PIKG---RK 310
QY 229 INWLKGGIITAAKLVTVSPNYATEIAADAAGGVDELTVIRAKGLEGVINGMDIEWPNKT 288
Db 311 INNMKAGIIESRALTVSPYQAQLLSGEERGVDELNLRVTSTITGVINGMDVNEWPNPT 370

QY 289 DKFLSAPYDONSIVYAGKAAKEALQALGLPVDPTAPLFAFICGRLEKQGVDIILALPK 348
Db 371 DKVITYADATTWEAKPLNKEALQALGLPVDPTAPLFAFICGRLEKQGVDIILALPK 430
QY 349 ILATPVOIALTGKAAEKLVAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVPSR 408
Db 431 FF-DQDVQVIVLGTGKKLERQALLDEDFDKRAHMKFNIPLAHIMAGADILVIPS 489
QY 409 FEPCLGLIQLHAMHYGTVPVAVASTGGLVDTVKEGVTGFMHGM--ALNPKLDEADADALAAT 466
Db 490 FEPCLGLIQLQCMQYGTFSACSSSTGGLVDTVKEGVTGFMHGFSAFCEVVDLSLVKKV 549
QY 467 VRASEVPAGGRYPPEMVAVANCISODLSWSKPAQKWEGLL-----EENVYKGGVATAK 518
Db 550 VKRALMVIYGTGTPAFEMTQNCMAQDLSWKGPAKNEQVLLNL-----GVAGSEPGYDGEI- 608
QY 519 KEEKVP 525
Db 609 KENVATP 615

RESULT 7
US-08-836-567-10
; Sequence 10, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-567-10

Query Match 32.6%; Score 902.5; DB 4; Length 641;
Best Local Similarity 39.8%; Pred. No. 2.8e-83;
Matches 212; Conservative 90; Mismatches 161; Indels 69; Gaps 19;

COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196.390
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 21 588.9
FILING DATE: 29-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 36 917.7
FILING DATE: 11-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02793
FILING DATE: 28-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-196-390-2

```

Query Match      31.7%; Score 878; DB 4; Length 671;
Best Local Similarity 39.9%; Pred. No. 9.6e-81;
Matches 210; Conservative 78; Mismatches 164; Indels 74; Gaps 16;

QY      4  IVVAAEVAWPSKTTGGIGDVTGGPIELVKRGHRVMTIAPRY-----DOYADAWDTSVV 57
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY     58  VDIM----GBKRYIFHSIKKGVHRVWDHPWF LAKVWGKTGSKLIYGRSGADYLDNKHRF 113
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    116  IKIPCGGSHVETFFHEYRDNVDWVFVDPH-----SYHRPGS-LYGNFPGA-FGDNQFRY 168
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    114  ALFCKAAIEAARVLFPGP-----GEDCVFVNDWHSALVPVLLKDYQPKGQFTKAKSVLAI 170
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    169  TLLCYACEAPLILELGGYTYGQNCWFVNDWHSALVPVLLAAARIYTVGTRDSRSLVI 228
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    171  HNIAFGQRMEEAEFKLPOAAFPDKLAFSDGYAKVYTEATPMEDEKPPLTGTYYKKIN 230
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    229  HNLHQGVEPASTYDGLGLPEWKGLEW-----VFPWARRRHALDKG-----EAVN 275
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    231  WLKGHIIAADKLVTVSFNPAIETAAADAGGVELDTVI--RAKGLEGIVNGMDIEWPNKT 288
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    276  FLKGAVVTADRIVVSQCYSEWVTT-ABGGGGLNELLSSRSKSVGLNGLVINGIDINDWNPIT 334
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    289  DKFLSAPYDQNSVYAGKAAAEALQAEILGLPVDTPALFAFGLKEQKGVDIILAALPK 348
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    335  DKCLPHYSVDLL-SGRAKKAEILQELGLRPREDVPLIGIGRLDTQKGLIDLKMAIPE 393
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    349  ILATPKVQIALIGTGKAAEYKLVNAIGTYKGRAGVYVKFSAPLAHMLTAGADEFMLVPSR 408
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    394  LM-REDYQFVLMGSDPIFEQWMRSTESSYKDKFRGWGVGFVSPVSHRITAGCDILLMPSR 452
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    409  FEPGCLIQIHAMHYGTVPVAVASTGGLVDTVK-----EGVTGFHMGALNPDKLDEAD 459
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    453  FEPCCGLNOLYAMQYGVFVHVGTGGLRDTVETFNFPFGAKGBEGTGWAFSPITVDKMLWA- 511
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    460  ADALAAATVRRASEVFAGKRYPEMVANCISQDLSWSKPAQKWEGGLE 505
DB      11  |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 512 -----LRTAMSTFRE-----HKPS--WEGLMK 533

RESULT 10
US-09-388-743-26
; Sequence 26, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Ian
; TITLE OF INVENTION: No. 6423886el Starch Synthese Polynucleot
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 801
; TYPE: PRT
; ORGANISM: Typha latifolia
US-09-388-743-26

Query Match	31.5%	Score	873	DB	4	Length	801		
Best Local Similarity	38.9%	Pred.	No. 4.2e-80						
Matches	211	Conservative	79	Mismatches	166	Indels	86	Gaps	16
QY	2	LDIVMVAEAPWSKTGGLGVDVTGGLPTIELYKRGHRVMTIAPRDYDQYADADMTSV--VVD	59						
DB		226	MNIIVAAECAPWSKTGGLGVDYAGALPKALARRGHRVMVAPRGYNAEPQDIGVKYK	285					
QY	60	IMGE--KYRYPHSIKKGVRVWIDHPWFLAKVWGKTGSKLY-GRPSGADYLDNKHRRFALF	116						
DB		286	VHGQDMVEYTHAYIDGVDFVFMDSDFRHR-----GNRIYEGNR-----VDILKRMILF	335					
QY	117	CKAATEAARVLP-----FGPGEDCVFVANDWHSALVPVLLKDEYQKGFQKAKSVLAIH	171						
DB		336	CKAAEYVPHVPCGGFCYGDG-NLAFIINDHETALLPYLKAYIRDNLGMLKYARSVLVIH	394					
QY	172	NIAFOGRMEFAFKDTKLPOAFAFKLAFSDGYAKVYVTEATPMEDEKPLPGTKYKKNW	231						
DB		395	NIAHOGRGVDDDFKFGVLPDHYLDLFLYD-----PVGG-----EHLNI	433					
QY	232	LKGIIADKLVTYSPNATETATAADAGGVLDTVIRAKG--IEGIVNGMDIEEWNPKTD	289						
DB		434	FAAGLKTADRVVTVSHGYAWELKT--SEGQWGLHEIINESNKKFGQIVNGIDAKESPFED	492					
QY	290	KFLSAP-----YDONSYYAGKAAAKEALQAEGLPVDPTAPLFAFGRLEEQKGVDIILAA	345						
DB		493	VHLKSDGYTNSLSDYLEMGKPVCKAALQREVGLPVRDNPVPIIAFIRGLDHQGVDLIAEA	552					
QY	346	LPKILATPKVQJAILGTGKAAEYKELVNAIGTYIKGRAGVKVFKSAPLAHMLTAGADFMLV	405						
DB		553	MPWIV-SHDVQVVMGLGTGRQDLLENLRNPEGGHRDKRAWVAFSVKMAHRIITAGADILMM	611					
QY	406	PSRFEPGGLIOLHAMHYGNVPVYASTGGVLVDVVKEGVTGFHMGALNPDKLDEADADALAA	465						
DB		612	PSRFEPGGLNQLYAMMYGIPIPVVHVGGLRDIVTQ-----FDFNESGLGW	657					
QY	466	TVYRASEVFAFGRYPEMVA NCIS-----ODLSNKPAPQAKWEGILLIEV	507						
DB		658	TEDRAE---AGKLIHALNCLNTYNYKDSNKGQLQTRGMQDLSDWNAAQYEDVLVAA	713					
QY	508	VY	509						
DB		714	KY	715					

RESULT 11
US-08-836-567-8
; Sequence 8, Application US/08836567
; Patent NO. 6130367
; GENERAL INFORMATION:

```

; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCI/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agreevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 767 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-836-567-8

```

Query Match 31.5%; Score 871; DB 4; Length 767;

Best Local Similarity 39.7%; Pred. No. 6.2e-80;

Matches 210; Conservative 78; Mismatches 181; Indels 60; Gaps 14;

QY 2 LDIVVAAEVAWPSKGTGLGDTGGPIELVKGHRVMTIAPRYDOYADAWDSV---V 57

DB 276 MNIIVASECAPWSKGTGLGDTGGALPKALARRGHRVMVAPRYDNPEDSGVRKIYK 335

QY 58 VDIMGEKVRYFHSIKKGVHVRWIDHPWFLAKVKGKTSKLYGPRSGADYLDNHNKRFALFC 117

DB 336 VDGQDVETIYFQADIGDVFVFD-----SHMERHIGNNIY-----GGRVVDILKRMVLF 386

QY 118 KAAIEAARVLP-----FGPCEDCVFVANDHWSALVPLVKDEYQPKGQFTKAKSVLAHN 172

DB 387 KAAIEVPWHPVCGVCYGDG-NLVFTANDHWTALLPVYLYKAYYRONGIMNYSRLVHN 445

QY 173 IAPQGRWEEAFKDTKLPAQAFDKLAFSDGYAKVYTEATPMEDEKPPITGKYKKNWL 232

DB 446 IAHQGRPLEDFSVDLPVPHYMDPKLYD-----PVCGEHF---NIF 484

QY 233 KGGIADKLIVTSPNPKATEIAADAAGELDTVIRAKG---IEGIVNGMDIEEWNPKTDK 290

DB 485 AAGLKATADVTVVSHGYSWELKT-SQGGWGLHOLINENDWKLOGIYNGIDTKWNPEDLY 543

QY 291 FLISAP-----YDONSVVYAGAAKAEALQAEGLPVDPTAPLFAFIEGKQGVDDIILAL 346

DB 544 HLOSDGMYNSLDTLGTGPKQKAAALQKELGVPVRDDVPLIGFIGIDLPQKGVLDIAEAS 603

QY 347 PKILATPKVQIALLGTGKAAEKLVAIGTKYKRAKGVVKSAPLAHMLTAGADFWIYP 406

```

DB 604 ANWMMG-QDVQLVMLGTGRRDLQMLRFQECQHNDKIRGWGFSVKTSHRITAGADILLMP 662
QY 407 SRFEPCCGLIQLHAMVGTVPVAVSTGGLYDVTVK-----EGVTGFHMGALNPKDLDEADA 460
DB 663 SRFEPCCGQLYAMKYGIIPVHVAVGGLRDTVQFPDFPNESGLIGWTFSRAEASQLIHALG 722
QY 461 DALAATVRRASEVVFAGGRYPENVANCISODLSWSKPAQKWEGILLEVVY 509
DB 723 NCL-LTYREYKKSWEG-----IQTRCMTODLSWDNAAQNYEVLIAKY 765

```

RESULT 12

US-08-941-445A-21

; Sequence 21, Application US/08941445A

; Patent No. 6107060

; GENERAL INFORMATION:

; APPLICANT: Keeling, Peter

; APPLICANT: Guan, Hanping

; TITLE OF INVENTION: Starch Encapsulation

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

; STREET: 5370 Manhattan Circle

; CITY: Boulder

; STATE: CO

; COUNTRY: US

; ZIP: 80303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/941,445A

; FILING DATE: 30-SEP-1997

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/026,855

; FILING DATE: 30-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Winner, Ellen P

; REGISTRATION NUMBER: 28,547

; REFERENCE/DOCKET NUMBER: 89-97

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 499-8080

; TELEFAX: (303) 499-8089

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 539 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-941-445A-21

Query Match

Best Local Similarity 31.1%; Score 861.5; DB 3; Length 539;

Matches 194; Conservative 81; Mismatches 154; Indels 47; Gaps 13;

QY 4 IVVVAEVAWPSKGTGLGDTGGPIELVKGHRVMTIAPRY-----DOYADAWDSV 57

DB 51 IVFTGTGASPYAKSGGLGDCVCSLPLVLAARGHRVMVMPRYLNGTSDKNYANAFYTEKH 110

QY 58 VDIM--GE-KVRYFHSIKKGVHVRWIDHPWFLAKVKGKTSKLYGPRSGADYLDNHNKRF 113

DB 111 IRPCPGGEHEVFFHEYRDSVDVWFVDHPSY-----HRPGNLYGDKFGA-FGDNQF 163

QY 114 ALFCKAAIEAARVLPFGP---GEDCVFVANDHWSALVPLVKDEYQPKGQFTKAKSVLA 170

DB 164 TLACYAACEAPLILELGGIYQNCMFVNDHWSALVPLVLAARYPYGVYKDSRLVI 223

QY 171 HNTAFQGRWEEAFKDTKLPAQAFDKLAFSDGYAKVYTEATPMEDEKPPITGKYKKN 230

Db 224 HNLHQGVPEASTYDGLGPPWYGALW------VFPWARRHALDKG-----EAVN 270
 QY 231 WLKGGIIAADKLVTSPTYATEIAADAAGGVLDTVI--RAKIEGIVNGMDIEENPKT 288
 Db 271 FLKGAVVATADRIIVTSKGSWEVTT-AEGGQGLNELLSSRKSVLNGVINGIDINDWNPAT 329
 QY 289 DKFLSAPYDQNSVYAGKAAKAEALQALGLPVDPTAPLFAFIRLEEQKGVDIILAALEPK 348
 Db 330 DKCIPCHYSVDDL-SGKAKCKGALQKELGLPIRPDVPPLIGFIRGLDYQKGDILQLIIPD 388
 QY 349 ILATPKVQTAILGTGKAAAEKLVNAIGTKYKGRAGKGVVFKSAPLAHMLTAGADFMVLPSP 408
 Db 389 LM-REDVQFVMLGSGDPELEDWMRSTESIFDKFRGWGFSVPVSHRITAGCDILLMPSP 447
 QY 409 FEPCCGLIQLHAMHYGTVPPVASTGGGLVDTVK-----EGVTGFHMGALNPDKL 455
 Db 448 FEPCCGLNQLYAMQYGTVPVVAHTGGURDITVENFPFGENGEGQGTGWAFAPLITENN 503

RESULT 13

US-08-941-445A-13
 ; Sequence 13, Application US/08941445A
 ; Patent No. 6107060
 ; GENERAL INFORMATION:
 ; APPLICANT: Keeling, Peter
 ; APPLICANT: Guan, Hanping
 ; TITLE OF INVENTION: Starch Encapsulation
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 ; STREET: 5370 Manhattan Circle
 ; CITY: Boulder
 ; STATE: CO
 ; COUNTRY: US
 ; ZIP: 80303

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/941,445A
 ; FILING DATE: 30-SEP-1997
 ; CLASSIFICATION: 800

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/026,855
 ; FILING DATE: 30-SEP-1996

ATTORNEY/AGENT INFORMATION:
 ; NAME: Winner, Ellen P
 ; REGISTRATION NUMBER: 28,547
 ; REFERENCE/DOCKET NUMBER: 89-97
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 499-8080
 ; TELEFAX: (303) 499-8089
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 583 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-941-445A-13

Query Match 31.1%; Score 861.5; DB 3; Length 583;
 Best Local Similarity 40.8%; Pred. No. 3.7e-79;
 Matches 194; Conservative 81; Mismatches 154; Indels 47; Gaps 13;

QY 4 IVMYAAEAPWSKTGGLDVTGGLPIELVKRGHRVMTIAPRYDOYADADMTSVV 57
 Db 95 IVFVTGEASPYAKSGGLGDCVGLPVALAARGHRVMTIAPRYDOYADADMTSVV 154
 QY 58 VDIM--GE-KVRYPFHSIKKGVRVWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHRKFR 113
 Db 155 IRIPCFGGEHEVTFEYRDSVDWVFDHPSY-----HRPGLNYGDKFGA-FGDNQPRY 207

QY 114 ALFCKAAIIPAARVLPFGP---GEDCVFVANDWESALVPVLLKDEYQPKGQFTKAKSVLAI 170
 Db 208 TLCLYAAACEAPLIIELGGYIYQNCMFVVDWFEASLPVLLAAKARYPYGVYKDSRSILVI 267
 QY 171 HNTAFQGRWMEAEAFKTKLPQAAFDKLAESDGYAKVYVTEATPWEDEKPLTKTKYKKN 230
 Db 268 HNLHQGVPEASTYDGLGPPWYGALW------VFPWARRHALDKG-----EAVN 314
 QY 231 WLKGGIIAADKLVTSPTYATEIAADAAGGVLDTVI--RAKIEGIVNGMDIEENPKT 288
 Db 315 FLKGAVVATADRIIVTSKGSWEVTT-AEGGQGLNELLSSRKSVLNGVINGIDINDWNPAT 373
 QY 289 DKFLSAPYDQNSVYAGKAAKAEALQALGLPVDPTAPLFAFIRLEEQKGVDIILAALEPK 348
 Db 374 DKCIPCHYSVDDL-SGKAKCKGALQKELGLPIRPDVPPLIGFIRGLDYQKGDILQLIIPD 432
 QY 349 ILATPKVQTAILGTGKAAAEKLVNAIGTKYKGRAGKGVVFKSAPLAHMLTAGADFMVLPSP 408
 Db 433 LM-REDVQFVMLGSGDPELEDWMRSTESIFDKFRGWGFSVPVSHRITAGCDILLMPSP 491
 QY 409 FEPCCGLIQLHAMHYGTVPPVASTGGGLVDTVK-----EGVTGFHMGALNPDKL 455
 Db 492 FEPCCGLNQLYAMQYGTVPVVAHTGGURDITVENFPFGENGEGQGTGWAFAPLITENN 547

RESULT 14

US-09-388-743-6
 ; Sequence 6, Application US/09388743
 ; Patent No. 6423886

GENERAL INFORMATION:
 ; APPLICANT: Singletary, George

APPLICANT: Zhou, Lan
 ; TITLE OF INVENTION: No. 6423886el Starch Synthese Polynucleotides and Their

FILE OF INVENTION: Use in the Production of New Starches

FILE REFERENCE: 1144

CURRENT APPLICATION NUMBER: US/09/388,743

CURRENT FILING DATE: 1999-09-02

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6

LENGTH: 690

TYPE: PRT

ORGANISM: Curcuma zedoaria

US-09-388-743-6

Query Match 31.0%; Score 858; DB 4; Length 690;
 Best Local Similarity 39.0%; Pred. No. 1.1e-78;
 Matches 208; Conservative 80; Mismatches 176; Indels 70; Gaps 15;

QY 2 LDIVWAAEAPWSKTGGLDVTGGLPIELVKRGHRVMTIAPRYDOYADADMTSVV---- 57
 Db 199 MNIILVAEAPWSKTGGLDVTGGLPIELVKRGHRVMTIAPRYDOYADADMTSVV---- 258
 QY 58 VDIMEKVRYPFHSIKKGVRVWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHRKFRALFC 117
 Db 259 VDGQDMEIKYTHYTIIDSVDFEIDSP-----IFRIGNDIY-----GGNRVDILKEMVLF 309
 QY 118 KAAIEAARVLP-----FGGEDCVFVANDWESALVPVLLKDEYQPKGQFTKAKSVLAIHN 172
 Db 310 KAAVEVPWHVPCGGFCYGDG-NLVFTANDWHTSLPVPVYLKACFRDRGLMTYARCILLVHN 368
 QY 173 IAFQGRWMEAEAFKTKLPQAAFDKLAESDGYAKVYVTEATPWEDEKPLTKTKYKKNWL 232
 Db 369 IAHQGRPLDDFVYVDLPHDLHLDSPRDD-----PVGSEHF---NLF 407
 QY 233 KGGIIAADKLVTSPTYATEIAADAAGGVLDTVIIRA--KGIEGIVNGMDIEENPKTKDK 290
 Db 408 AAGTAAADRVTYVSHGYAWELKT-SEGCGWGLHELINECHWKPHGVINGIDTSHWNPKEA 466
 QY 291 FLSAP-----YDONSVYAGKAAKAEALQALGLPVDPTAPLFAFIRLEEQKGVDIILAA 346
 Db 467 HLNSDGYNTFTLETLEMGKAOCKAALQREFGLFVPRDDVPILAFIRGLDHQKGDILTAEM 526

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 4, 2003, 14:56:21 ; Search time 16.3988 seconds
(without alignments)
3342.965 Million cell updates/sec

Title: US-09-980-771A-9

Perfect score: 2769

Sequence: 1 ALDIVMAAEVAPWSKTGGL.....GGVATAKKEIKVPVAKIP 531

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCI_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCITUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1450.5	52.4	636	9	US-10-138-075-4
2	1433.5	51.8	609	9	US-10-138-075-2
3	1379	49.8	599	9	US-10-138-075-5
4	878	31.7	671	10	US-09-952-677-2
5	841	30.4	799	10	US-09-952-677-6
6	555	20.0	915	9	US-10-163-214-6
7	549	19.8	914	9	US-10-163-214-12
8	545	19.7	909	9	US-10-163-214-2
9	537	19.4	874	9	US-10-163-214-13
10	410.5	14.8	474	12	US-10-007-693-99
11	402.5	14.5	476	12	US-10-007-693-69
12	385.5	13.9	293	9	US-10-163-214-10
13	215.5	7.8	117	10	US-09-739-438-2
14	206	7.4	409	9	US-09-738-626-4738
15	189	6.8	381	9	US-09-738-626-5896
16	164	5.9	143	10	US-09-739-438-4
17	155.5	5.6	191	10	US-09-924-358-22
18	155.5	5.6	418	9	US-09-738-626-3951
19	136.5	4.9	385	10	US-09-767-041-18

20	126	4.6	387	9	US-09-738-626-3890	Sequence 3890, Ap
21	125.5	4.5	398	10	US-09-934-899-16	Sequence 16, Appl
22	125.5	4.5	398	10	US-09-934-868-36	Sequence 36, Appl
23	124	4.5	379	9	US-09-738-626-6655	Sequence 6655, Ap
24	123.5	4.5	413	9	US-09-738-626-4025	Sequence 4025, Ap
25	118.5	4.3	372	10	US-09-815-242-5277	Sequence 5277, Ap
26	118.5	4.3	384	10	US-09-815-242-12605	Sequence 12605, A
27	117.5	4.2	636	9	US-09-738-626-5590	Sequence 5590, Ap
28	114.5	4.1	2993	9	US-09-738-626-6239	Sequence 6239, Ap
29	110.5	4.0	121	9	US-10-163-214-4	Sequence 4, Appli
30	108	3.9	802	9	US-10-080-114A-2	Sequence 2, Appli
31	108	3.9	809	9	US-10-080-114A-12	Sequence 12, Appl
32	106	3.8	718	10	US-09-815-242-12915	Sequence 12915, A
33	106	3.8	802	9	US-10-080-114A-5	Sequence 5, Appli
34	105.5	3.8	490	9	US-10-218-743-41	Sequence 41, Appl
35	105.5	3.8	509	9	US-10-218-743-35	Sequence 35, Appl
36	105.5	3.8	509	9	US-10-218-743-38	Sequence 38, Appl
37	105.5	3.8	1156	10	US-09-815-242-13187	Sequence 13187, A
38	105	3.8	195	10	US-09-815-028-8	Sequence 8, Appli
39	104.5	3.8	732	10	US-09-381-624A-3	Sequence 3, Appli
40	102.5	3.7	489	10	US-09-815-242-11953	Sequence 11953, A
41	102.5	3.7	805	9	US-10-137-036-77	Sequence 77, Appl
42	102	3.7	3816	9	US-09-808-880-3	Sequence 3, Appli
43	101.5	3.7	1164	10	US-09-870-122-1	Sequence 1, Appli
44	99	3.6	562	9	US-09-712-363-254	Sequence 254, App
45	98.5	3.6	448	9	US-09-738-626-3991	Sequence 3991, Ap

ALIGNMENTS

RESULT 1

US-10-138-075-4
; Sequence 4, Application US/10138075
; Publication No. US20030087369A1
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Orozco, Emil M.
; TITLE OF INVENTION: Granule-Bound Starch Synthase
; FILE REFERENCE: BRL474 NA
; CURRENT APPLICATION NUMBER: US/10/138,075
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/288,315
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Glycine max
US-10-138-075-4

Query Match	52.4%	Score 1450.5;	DB 9;	Length 636;
Best Local Similarity	53.0%	Pred. No. 6.3e-113;		
Matches	291;	Conservative	71;	Mismatches 144;
				Indels 43; Gaps 10;
QY	2	LDIVMAAEVAPWSKTGGLGVGGGLPIELVVKGRHYMTIAPRYDOYADAMDTSSVVDI-	60	
Db	106	MTPIITIGTEVAPWCKTGGLGVGGGLPALAGFGRHYMTIVPRYDQYKDAWDTSSVLEVK	165	
QY	61	--MGEKRVFHSHTKGVHRVWIDHPWFLAKVWCKTSKLYGPRSGADYLDNKKRFLFC	117	
Db	166	VGRTKRVFFHCYKRGVDRVFDHPFWLEKVKGTGLYGTGTGNDYEDNQLRSLFC	225	
QY	118	KAAIEARVLDPF-----GP-GEDEVFANDHWSALVPVLLKDEYQPKQGFKAQSVLA	169	
Db	226	QAALAPRVLNLSNYSFSGPYGEDYIFVANDHNTALIFCYLKSVMYQSGRIYINARVVF	285	
QY	170	IHNIAQGRWWEAFDKTKLPQAAFDKLAFSQYAKVYTEATPMEDEKPLFGKTYKKI	229	

Db 286 IHNIAYQGRFAFADESLINLPDQKSSFDIDGHVK-----PVVG---RKI 328
 QY 230 NWLKGIIIAADKLIVTSPNYATEIAADAAGGVELDTVIRA-----KGIEGIVNGMOTEEWN 285
 Db 329 NWLKGIIIESWFTVITVSPNYAKELVSGDPKGVELDNIIRKIIDDDGRLVGIIVNGMDVQEW 388
 QY 286 PKTDKPLSAPYQNSYAGKAAKEALQAEGLGVPDPTAPLFAFAGRLSEOKGVDIILAA 345
 Db 389 PITDKVIAYKYDVSTVLEAKALLKEALQAEVGLPVDNIPNLIGFIGRLEOKGSDILAEA 448
 QY 346 LPKILATPKVQIALTGTGAAYEKUNATGTYKGRAGKGVVKSAPLAHMLTAGADFMV 405
 Db 449 IPOFI-KONVOLVALGTGKQMEKOLELEISYPDKARGVAKFNVPLAHMIIAGADFI 507
 QY 406 PSRFEPCGLIOLHAMHYGVPPVASTGGGLVDIVTKEGVTGFHMGALNP--DKLDEADADAL 463
 Db 508 PSRFEPCGLIOLQAMRYGSPVIVASTGGGLVDIVTKEGVTGFHMGALNP--DKLDEADADAL 567
 QY 464 AATVRRASEYFAGGRYPPEMVCANGISQDLSWSKPAQKWEGLLEVVY-----GKG--VAT 516
 Db 568 SKTVKRALAVYGPFAFTEIILKNCAQDLSWKPAKEWEVLLSLGVPGSPGSDGEIAP 627
 QY 517 AKKEIKVP 525
 Db 628 QAKENVATP 636

RESULT 2
 US-10-138-075-2
 ; Sequence 2, Application US/10138075
 ; Publication No. US20030087369A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Broglie, Karen E.
 ; APPLICANT: Butler, Karlene H.
 ; APPLICANT: Harvell, Leslie T.
 ; APPLICANT: Lightner, Jonathan E.
 ; APPLICANT: Orozco, Emil M.
 ; TITLE OF INVENTION: Granule-Bound Starch Synthase
 ; FILE REFERENCE: BB1474 NA
 ; CURRENT APPLICATION NUMBER: US/10/138,075
 ; CURRENT FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: 60/288,315
 ; PRIOR FILING DATE: 2001-05-03
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 2
 ; LENGTH: 609
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 US-10-138-075-2

Query Match 51.8%; Score 1433.5; DB 9; Length 609;
 Best Local Similarity 52.3%; Pred. No. 1.6e-111;
 Matches 288; Conservative 75; Mismatches 139; Indels 49; Gaps 11;

QY 2 LDIWVAEAPWSKTGGLGVDVTGGLPIELVKRHRVMTIAPRYDOYADADWTSVVDI- 60
 Db 81 MTIVFATEVHPWCKTGGLGVDVGGGLPPALAAAGHRVMTIAPRYDOYKDAWDTSLIVEVN 140
 QY 61 MG---EKVRYFHSIKKGVRHWIDHPWFLAKVWGTGSKLYGPRSGADYLDNKKRFALFC 117
 Db 141 IGDIVETVRFHCYKRGVDRVFDVHPMFLKVKWGTGAKLYGPTTGTDYRONQLRFLC 200
 QY 118 KAAIEAARVLPF-----GP-GEDCVFVANDHWSALVPVLLKDYQPKGQFTKAKSVLA 169
 Db 201 LAALAPRVNLNNSEYSGYGEDVVEVANDHWTAILPCYLKSMYKENGIVYKNAKAVFC 260
 QY 170 IHNIAYQGRMWEAFKDKLPQAAFDKLAFSYGAKVYVTEATPMEDEKPLTGTGYKI 229
 Db 261 IHNIAYQGRFARADELLNPDSELPSPDFIDGHVK-----PVVG---RKL 303
 QY 230 NWLKGIIIAADKLIVTSPNYATEIAADAAGGVELDTVIRA-----KGIEGIVNGMOTEEWNPKT 288

Db 304 NWMKAGIIISDLVLTSPHYVVKELTSGDPKGVGLDGLVLRKTKPLEIGIVNGMDVEMDPST 363
 QY 289 DKFELSPYQNSYAGKAAKEALQAEGLGVPDPTAPLFAFAGRLSEOKGVDIILAA 348
 Db 364 DKYISAKYDATTVEARALNKERLQAEVGLPVDSSIPVIVFVGRLEEQKSGDILIAAIE 423
 QY 349 ILATPKVQIALTGTGAAYEKUNATGTYKGRAGKGVVKSAPLAHMLTAGADFMVPSR 408
 Db 424 FVG-ENVOIILVLTGTKKKMEELTQLEVKYPPNARGIAKENVPLAHMFAFADFIIVPSR 482
 QY 409 FEPGGLIOLHAMHYGVPPVASTGGGLVDIVTKEGVTGFHMGALNP--DKLDEADADAL 466
 Db 483 FEPGGLIOLQAMRYGVPICSSITGGGLVDIVTKEGVTGFHMGSEFVECEVTPADVAVAST 542
 QY 467 VRRASEYFAGGRYPPEMVCANGISQDLSWSKPAQKWEGLLEVVYVKG-----GV 514
 Db 543 VTRALKQYDTPAFHEMVCANGISQDLSWSKPAQKWEGLLEVVYVKG-----GV 514
 QY 515 ATAKKEIKVP 525
 Db 599 APLAKENVATP 609

RESULT 3
 US-10-138-075-5
 ; Sequence 5, Application US/10138075
 ; Publication No. US20030087369A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Broglie, Karen E.
 ; APPLICANT: Butler, Karlene H.
 ; APPLICANT: Harvell, Leslie T.
 ; APPLICANT: Lightner, Jonathan E.
 ; APPLICANT: Orozco, Emil M.
 ; TITLE OF INVENTION: Granule-Bound Starch Synthase
 ; FILE REFERENCE: BB1474 NA
 ; CURRENT APPLICATION NUMBER: US/10/138,075
 ; CURRENT FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: 60/288,315
 ; PRIOR FILING DATE: 2001-05-03
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 5
 ; LENGTH: 599
 ; TYPE: PRT
 ; ORGANISM: Triticum aestivum
 US-10-138-075-5

Query Match 49.8%; Score 1379; DB 9; Length 599;
 Best Local Similarity 50.4%; Pred. No. 5.5e-107;
 Matches 277; Conservative 78; Mismatches 147; Indels 48; Gaps 10;

QY 2 LDIWVAEAPWSKTGGLGVDVTGGLPIELVKRHRVMTIAPRYDOYADADWTSVVDI 61
 Db 72 MPILFATEVHPWCKTGGLGVDVGGGLPPALAAAGHRVMTIAPRYDOYKDTWDTNVLVEVI 131
 QY 62 ---GEKRYFHSIKKGVRHWIDHPWFLAKVWGTGSKLYGPRSGADYLDNKKRFALFC 117
 Db 132 VGDRTETVRFHCYKRGVDRVFDVHPMFLKVKWGTGSKLYGPTTGTDYRONQLRFLC 191
 QY 118 KAAIEAARVLPF-----GP-GEDCVFVANDHWSALVPVLLKDYQPKGQFTKAKSVLA 169
 Db 192 LAALAPRVNLNNSEYSGYGENVVFVANDHWTAVLPCYLKSMYKONGIYVNAKAVFC 251
 QY 170 IHNIAYQGRMWEAFKDKLPQAAFDKLAFSYGAKVYVTEATPMEDEKPLTGTGYKI 229
 Db 252 IHNIAYQGRFPRVDFELNLPSEFDFVGHVK-----PVVG---RKL 294
 QY 230 NWLKGIIIAADKLIVTSPNYATEIAADAAGGVELDTVIRA-----KGIEGIVNGMOTEEWNPKT 288
 Db 295 NWMKAGIIECDVLLVITVSPHYVVKELTSGDPKGVGLDGLVLRKTKPLEIGIVNGMDVEMDPST 354
 QY 289 DKFELSPYQNSYAGKAAKEALQAEGLGVPDPTAPLFAFAGRLSEOKGVDIILAA 348

Db 355 DKYISVKNATTVAEARLNKEILQAEVGLPVDSSIPVIVFICRLEEQKSGDILLIAAIP 414
QY 349 ILATPKVQIAIIGTCKAAEKLVAIGTKYKRAKGVVKSAPLAHMLTAGADEMLVPSR 408
Db 415 FL-ENVOVLIVGTGKKWKEELMLEAKYIPONAKGIKFNPLAHMFAGANFIIVPSR 473
QY 409 FEPCLGILHMHYGTVPVASTGGIVDVRVKEGVTGFHMGALNP--DKLDERADALAAAT 466
Db 474 FEPCLGILQGRYGVIPICSTGGIVDIVSEGVTFHMGSGVNFETVDPADVAASVN 533
QY 467 VRRASEVAGGRYPPEMVANCISQDLSWSKPAQKWEGLLEEVYVYKRG-----GVA 515
Db 534 VTRALKQYKTPSFHAMVONCMAQDLSWKGPAKKW-----EALLGLGVESQPGIEGEETA 589
QY 516 TAKKEEIKVP 525
Db 590 PLAKONVATP 599

RESULT 4

US-09-952-677-2

; Sequence 2, Application US/09952677

; Patent No. US20020138876A1

; GENERAL INFORMATION:

; APPLICANT: Block, Martina

; Lorz, Horst

; Lutticke, Stephanie

; Walter, Lennart

; Froberg, Claus

; Kossmann, Jens

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES

; FROM WHEAT WHICH ARE INVOLVED IN STARCH

; SYNTHESIS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/952,677

; FILING DATE: 14-Sep-2001

; PRIORITY INFORMATION DATA:

; APPLICATION NUMBER: 09/196,390

; FILING DATE: 19-No. US20020138876A1-1998

; APPLICATION NUMBER: DE 196 21 588.9

; FILING DATE: 29-MAY-1996

; APPLICATION NUMBER: DE 196 36 917.7

; FILING DATE: 11-SEP-1996

; APPLICATION NUMBER: PCT/EP97/02793

; FILING DATE: 28-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Haley, Jr., James F.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: AGREVO-9

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 596-9000

; TELEFAX: (212) 596-9090

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 671 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-952-677-2

Query Match 31.7%; Score 878; DB 10; Length 671;
Best Local Similarity 39.9%; Pred. No. 5.3e-65;
Matches 210; Conservative 78; Mismatches 164; Indels 74; Gaps 16;

QY 4 IVWAAREVAPWKTGGTGLDVTGGLPTELKVRGRHVMTIAPRY-----DOYADAWDTSVV 57
Db 56 IVFTVEAAPYAKSGGLGDCVSLPTALAAARGHRVVMVPRYLNGSSDKNYAKALYTAH 115
QY 58 VDIM-----GEKYRYFHSIKKGVRVWIDHPWFLAKVWGKSGKLYGPRSGADYLDHNRK 113
Db 116 IKIPCGGSGHEVTFHFHEYNDVNDWVFDHP-----SYHRPGS-LYGNDFCA-PGDNQFRY 168
QY 114 ALFCKAAIEAARVLPFGP---GEDCVFVANDHSAIVPVLLKDEYQPKQFTKAKSVLAI 170
Db 169 TLICYAACEAPLILELGGVYIYQNCMFVNDHSAIVPVLLAAKYRYPYGYRDSRSTLVI 228
QY 171 HNIATQGRMWEERAFKDKLPQAAFKLAFSDGYAKYVYTEATPMEDEKPLGKTYKIN 230
Db 229 HNLAHQGVPEASTYPLDGLPPEWYGALEW-----VPEWARRHALDKG-----EAVN 275
QY 231 WLKGGILAADKLVTYSPNYATEIAADAAGVVELDVI--RAKGIEGIVNGMDIEENPKT 288
Db 276 FLKGAVTADRLVTVSQGSWEVTT-AEGGQGLNELLSRKSVLNGIVNGIDINDWNPPT 334
QY 289 DKLSAPYDQNSVYAGKAAAKEALQAEGLPVDPTAPLFAFGRLEEQKGVDDIILAALEPK 348
Db 335 DKCLPHYSVDDL-SGKAKCAELQELGLPVREDVPLIGFGRLDYQKIDILIKMAIPE 393
QY 349 ILATPKVQIAIIGTCKAAEKLVAIGTKYKRAKGVVKSAPLAHMLTAGADEMLVPSR 408
Db 394 LM-REDVOFVMLGSGDPIFEGWMRSTESSYKDKFRGWGFSVPVSHRITAGCDILLMPSR 452
QY 409 FEPCLGILHMHYGTVPVASTGGIVDVTYK-----EGVTGFHMGALNPDKLDEAD 459
Db 453 FEPCLGILHMHYGTVPVASTGGIVDVTYK-----EGVTGFHMGALNPDKLDEAD 459
QY 460 ADALAAVRRASEVFAGGRYPPEMVANCISQDLSWSKPAQKWEGLLE 505
Db 512 -----LRTAMSTERE-----HKPS--WEGLMK 531

RESULT 5

US-09-952-677-6

; Sequence 6, Application US/09952677

; Patent No. US20020138876A1

; GENERAL INFORMATION:

; APPLICANT: Block, Martina

; Lorz, Horst

; Lutticke, Stephanie

; Walter, Lennart

; Froberg, Claus

; Kossmann, Jens

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES

; FROM WHEAT WHICH ARE INVOLVED IN STARCH

; SYNTHESIS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/952,677

; FILING DATE: 14-Sep-2001

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-163-214-12

Query Match 19.8%; Score 549; DB 9; Length 914;
Best Local Similarity 30.8%; Pred. No. 2.7e-37;
Matches 169; Conservative 89; Mismatches 202; Indels 88; Gaps 22;
QY 2 LDIVVAAEAPWPSKGTGLGVDVGTGLPIELVYKRGHVRMTIAPRYD-QYADAWDTSVVVDI 60
Db LHIAHIAEMAPVAVKVGGLADVISGLKALOKKGLHVEILPKYDCMQVQVSNLKLVDV 480
QY 61 MGEKRYFHSIKKGVHRVWIDHPWFLAKVWGKT--GSKLY--GPR-----SGADYLDNH 110
Db LVQS--YF-----EGNPNKIKWTGTVGELPVYFIEPQHAPMFTSRAQYYGEH 526
QY 111 ---KRALPCKAAIEAARVLPFGGEDC-VFVANDWHSALVPVLKDEYQPKGQFTKAKS 166
Db 527 DDFKRFYSFSAALE---LLYQSGKKVDIIHCHDWQTAFAVAPLYWDVYANLG-FNSARI 581
QY 167 VLATHNIAFOGRMWEAEAFKDTKLPOAADFCLAFSDGYAKVYTEATPMEDEKPP-LTGKT 225
Db 582 CFTCHNEFYQG-----TAPARDLAWC-----GIDVHLDPRDRMDSN 619
QY 226 YKINLWKGIIAADKLVTSPNYATEIAADAAGGVELDTVIRAKGIEGVNGMDIEEWN 285
Db 620 HGRINAVKAVYSNIVTVPYALEVRSESGRGLQDTLVKHSKFLGILNGIDTDTWN 679
QY 286 PKDKFLSAPYDQNSVYAGKAAKEALQAEGL-PVDPTAPLFAFIRLEQKGVYDIIIA 344
Db 680 PCDRYLKQVYNADL-QCKAANKAALREQLNLASVPSQPLVGCITFLVAQKGVHLIRH 738
QY 345 ALPKILATPKVQJIALGTGKAAEKLVAIGTKYKGR-----VPEIQREFEGADHFNQNNIRLILKYDDALSHC 791
Db 739 AIYK-TAELGGQFVLLGSSP-----VPEIQREFEGADHFNQNNIRLILKYDDALSHC 791
QY 396 LTAGADFMVPSRPEPCGLIQLHAMHYGTVPVASTGGGLVDV---KEGVTGFHMGALN 451
Db 792 IYAASDMFVPSIPEPCGLITQMIAMRYGSPVIVKTTGGLNDSVDFDDETP---MEVRN 848
QY 452 PDKLDEADALATVRRASEVFAGGRYPPEMVANCISQDL-----SWSKPAQKWEGLLEE 507
Db 849 GFTFVKADEQGLSSAMERAFNCYT--RKPEVWKOLVOKDMTIDFSWDTISASQYEDIYKA 906
QY 508 VYKGGVA 515
Db 907 VARARAVA 914

RESULT 8
US-10-163-214-2
; Sequence 2, Application US/10163214
; Publication No. US20030097688A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Katherine H.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthase Isoform V
; FILE REFERENCE: Bb1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2

; LENGTH: 909
; TYPE: PRT
; ORGANISM: Zea mays
US-10-163-214-2

Query Match 19.7%; Score 545; DB 9; Length 909;
Best Local Similarity 29.4%; Pred. No. 5.8e-37;
Matches 159; Conservative 92; Mismatches 199; Indels 90; Gaps 20;

QY 2 LDIVVAAEAPWPSKGTGLGVDVGTGLPIELVYKRGHVRMTIAPRYD-QYADAWDTSVVVDI 60
Db LHIVHIAEMAPVAVKVGGLADVISGLKALOKKGLHVEILPKYDCMQHQNINLKLVDV 475
QY 61 MGEKRYFHSIKKGVHRVWIDHPWFLAKVWGKT--GSKLY--GPRSGADYL-----107
Db 476 -----VVKSYFEGNMFANKIWTGTVGELPVYFIEPQHGGFFWRAQYYGEH 521
QY 108 DNHRKRALPCKAAIEAARVLPFGGEDC-VFVANDWHSALVPVLKDEYQPKGQFTKAKS 166
Db 522 DDFKRFYSFSALE---LLYQSGKKVDIIHCHDWQTAFAVAPLYWDVYANLG-FNSARI 576
QY 167 VLATHNIAFOGRMWEAEAFKDTKLPOAADFCLAFSDGYAKVYTEATPMEDEKPP-LTGKY 226
Db 577 CFTCHNEFYQG-----IAPQDLAYCGLDVBELDRPDR--MRDNSH 615
QY 227 KKINLWKGIIAADKLVTSPNYATEIAADAAGGVELDTVIRAKGIEGVNGMDIEEWN 286
Db 616 GRINAVKAVYSNIVTVPYALEVRSESGRGLQDTLVKHSKFLGILNGIDTDTWN 675
QY 287 KDKFLSAPYDQNSVYAGKAAKEALQAEGL-PVDPTAPLFAFIRLEQKGVYDIIIAA 345
Db 676 STDRELFKQVYSANDLY-GKSANKAALRKQLKASTOASQPLVGCITRLVPQKGVHLIRH 734
QY 346 LPKILATPKVQJIALGTGKAAEKLVAIGTKYK--GRAGVWVFSAPLAHMLTAGADF 402
Db 735 YKITELEG-QFVLVSSPSVQHIORFEFEGADHFNQNNIRLILKYDDALSHC 793
QY 403 MLVPSRPEPCGLIQLHAMHYGTVPVASTGGGLVDV---KEGVTGFHMGAL 450
Db 794 FIVPSMEPCGLTQMIAMRYGSPVIVKTTGGLNDSVDFDDETPMEVRNGTFFL-----848
QY 451 NPKLDEADALATVRRASEVFAGGRYPPEMVANCISQDL-----SWSKPAQKWEGLLEE 506
Db 849 ---KADEQD---FGNALERAFNY--HRKPEVWKOLVOKDMKIDFSWDTISQYEEIYQK 900

RESULT 9
US-10-163-214-13
; Sequence 13, Application US/10163214
; Publication No. US20030097688A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Katherine H.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthase Isoform V
; FILE REFERENCE: Bb1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 874
; TYPE: PRT
; ORGANISM: Vigna unguiculata
US-10-163-214-13

Query Match 19.4%; Score 537; DB 9; Length 874;
Best Local Similarity 30.4%; Pred. No. 2.6e-36;
Matches 166; Conservative 85; Mismatches 191; Indels 108; Gaps 25;

Db 248 VNNPKTDPALAVQYDASLLSEPDVLTFFKKEENRAVLYEKLGISSD-YFPLLCVISRIVEE 306
QY 337 KG-----VDLIALPKILATPKVQVAILGTGKAAVEKLVNAIGTKYKGRAG-----VVK 387
Db 307 KGEPMKEIILHAMHESYA-----FILIGTSQ--NEVLNFEFNQLQDCCLASSPNIRLILD 359
QY 388 FSAPLAHMLTAGADFMVPSRPEPCGLIOLHAMHYGTVPVASTGGLVTVKEGVTGFM 447
Db 360 FNDPLARLYAADMICIPSHREACGLIOLIAMRYGTVPVIRKTKGLADTVIPGVNGFTF 419
QY 448 GALNPKDLDEADALAAATVRRASEVFAGGRYPYEMVANCISODLSWSKPAQKWEGLLEEV 507
Db 420 --FDTNFNE-----FRAMLSNAVT---YRQEPDWLNLIESG 453
QY 508 VYKGVGVATKKEELKV 524
Db 454 MLRASGLDAMAKHYVNL 470
RESULT 12
US-10-163-214-10
; Sequence 10, Application US/10163214
; Publication No. US20030097688A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karen H.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthase Isoform V
; FILE REFERENCE: BBL520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-163-214-10

Query Match 13.9%; Score 385.5; DB 9; Length 293;
Best Local Similarity 33.0%; Pred. No. 2.5e-24;
Matches 101; Conservative 59; Mismatches 115; Indels 31; Gaps 9;
QY 228 KINWLKGIITAADKLVTVPVSNYATEIAADAGGVDELDTVIRAKGIEGIVNGMDIEWNPK 287
Db 1 KINAVGAVVYSNITVTVPSTYALVRSSEGGRLQDTLKVHSRFLGILNGIDTWNPC 60
QY 288 TDRFLSAPYDONSYYAGKAAKALQALGL-PVDPTAPLEAFTRLEEQKGVDIILAL 346
Db 61 TDRLKQVYNAKL-QGKAANKALRQLNLASAYSQPLVGCITRLVAQKGVHLIRHAI 119
QY 347 PKILATPKVQVAILGTGKAAVEKLVNAIGTKYKGRA-----KGWVKSAPLAHMLT 397
Db 120 YK-TAELGGQVVLGSSP-----VPEIQREFEGIAHFQNNNIRILIKYDALSICII 172
QY 398 AGADFMVPSRPEPCGLIOLHAMHYGTVPVASTGGLVDTV-----KEGVTGFHMGALNPD 453
Db 173 AASDMFTVPSIFPCGLITOMIAMRYGVPVIRKTKGLNDSVDFDDTIP---MEVRNGF 229
QY 454 KLDEADALAAATVRRASEVFAGGRYPYEMVANCISQDL-----SWSKPAQKWEGLLEEVY 509
Db 230 TFKVADQGLUSSAMERAFNCYT--RKPEVKNQLVQKDMTIDFSWDTASQYEDIYQAVA 287
QY 510 KGKGA 515
Db 288 RARAVA 293

RESULT 13
US-09-739-438-2

; Sequence 2, Application US/09739438
; Patent No. US20020029394A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Thorpe, Cathy
; TITLE OF INVENTION: Homologs of Starch Synthase D01
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/739,438
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/171514
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-739-438-2

Query Match 7.8%; Score 215.5; DB 10; Length 117;
Best Local Similarity 46.6%; Pred. No. 1.1e-10;
Matches 41; Conservative 17; Mismatches 25; Indels 5; Gaps 1;
QY 356 QTAILGTG-----KAAYEKLVAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVPSRFE 410
Db 8 QVVLGSDPDHRIQDFTNLASKLHGEYHGRVKLCITYDEPLSHLIYAGADFLVPSMFE 67
QY 411 PCGLIOLHAMHYGTVPVASTGGLVDTV 438
Db 68 PCGLTQLTAMRYGSIPIVRKTKGLYDTV 95

RESULT 14
US-09-738-626-4738
; Sequence 4738, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4738
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4738

Query Match 7.4%; Score 206; DB 9; Length 409;
Best Local Similarity 27.2%; Pred. No. 4.2e-09;
Matches 83; Conservative 47; Mismatches 127; Indels 48; Gaps 15;
QY 210 ATPWEDE--KPPLTGTGYKKINML-KGGIADKLVTVSPNYPVATEIAADAGGVDELDTV 266
Db 129 AHSLEPDRPKREQLGGYDVSWSSEKNAMEYADAVTAVSARMKDSILA-AYPIEDNV 187

QY 267 IRAKIEGIVNGMDIEFWNPCKDKLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPL 326
Db 188 -----RVVLNGIDTLMQPR-----PTFDD-----AEDSVLRSLG--VDPQRPI 224
QY 327 FAFIGRLEQKGVDIILALPKILATPKVQJAILGTGKAAVE--KLVNAIGTKYKGRAG 384
Db 225 VAFVGRITRQKGVHELIKA--AALEDESQVLVLCAGAPDTPETAAARTTALVEELQAKREG 282
QY 385 VVKFSAPLA-----HMLTAGADFMVPSRPEPCGLIQLHAMHYGTVPVVAAGTGLVDTVK 439
Db 283 IFWVQDMLGDKDKIQEILTA-ADTFVCPESIYEPLGIIVLEAMACNTAVVASDVGGEV 341
QY 440 EGVGTG--FHMGALNPKLDEADADA---LAATVRRASEVFAGGRYPENMVANCISQDLSWS 494
Db 342 DGTIGALVHYDENDVEIFERDIAEAVNKMVADRETAAKFGLAGR--ERAIN----DFSWA 395
QY 495 KPAOK 499
Db 396 TIAQQ 400

RESULT 15

US-09-738-626-5896
; Sequence 5896, Application US/09738626
; Publication No. US20020197605A1

GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5896
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum

US-09-738-626-5896

Query Match 6.8%; Score 189; DB 9; Length 381;
Best Local Similarity 27.0%; Pred. No. 1e-07;
Matches 74; Conservative 43; Mismatches 95; Indels 62; Gaps 14;
QY 260 GVELD-----TVIRAKG-----IEGIVNGMDIEFWNPCKDKLSAPYDQNSVYAG 304
Db 138 GTEVDLVIVISQYTLRRLREKSAFGSHPTFHLPSGVGVKRFPTAT-----PED----- 184
QY 305 KAAAEALQAEGLPVDPTAPLFAFIGRLEQKGVDIILALPKILAT--PKVQJAILGTG 363
Db 185 ----KSAFRKKLGF--TDTTPVIACNSRLVPKPGQDLSLIKAMPQVIAARPDQALLIVSGS 238
QY 364 KAAEKLVAIGTKYKGRAGVVKFSAPLAHM-----LTAGADFMVPSR-----FEPC 412
Db 239 R--YESTLRLATDSQN----VKELGRLEYQDMINTLAAADIFAMPARTRGGLDVEGL 292
QY 413 GLIQLHAMHYGTVPVVAAGT--GGLVDTVKEGVGFHMGALNPKLDEADADALAAATVRRAS 471

Db 293 GIVYLEAQACQ--VPVIAGTSGGAPETVTP-ATGLVWEGSDVDKLSLEILLDDPIRRAA 350
QY 472 EVFAGGRYPENMVANCISQDLSWSKPAOKWEGGLE 505
Db 351 MGRAAGRAH-----VEAEWSWEIMGERLTWNILQ 377
Search completed: June 4, 2003, 15:15:37
Job time : 21.3988 secs